



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 132448**

**TO: James Schultz**  
**Location: rem/2d18/2c18**  
**Art Unit: 1635**  
**Monday, September 20, 2004**

**Case Serial Number: 09/227881**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**REM-1A59**  
**Phone: 571-272-2523**

**toby.port@uspto.gov**

### **Search Notes**

Examiner Schultz,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Toby Port

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STIC-Biotech/ChemLib

132448

mej

From: Schultz, James  
Sent: Tuesday, September 14, 2004 11:18 AM  
To: STIC-Biotech/ChemLib  
Subject: Seq Search 09/227,881

RECEIVED  
SEP 14 2004  
(STIC)

Hello,  
Could you please run a standard nucleotide sequence search on SEQ ID NO: 34 in the above entitled case?

Thanks,  
Doug Schultz

James Douglas Schultz, PhD  
AU 1635 (Biotechnology)  
Patent Examiner  
United States Patent and Trademark Office  
(Office) REM 2D18  
(Mail) REM 2C18  
(571) 272-0763

\*\*\*\*\*  
STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 12:16:22 ; Search time 19737 Seconds

(without alignments) 11575.271 Million cell updates/sec

Title: US-09-227-881-34

Perfect score: 5271

Sequence: 1 atcttgcagttaccctc.....tcgggcacgagccagcaagg 5271

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_hg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_hg\_hum:\*

31: em\_hg\_inv:\*

32: em\_hg\_other:\*

33: em\_hg\_mus:\*

34: em\_hg\_pln:\*

35: em\_hg\_rdg:\*

36: em\_hg\_mam:\*

37: em\_hg\_vrt:\*

38: em\_sy:\*

39: em\_hg\_hum:\*

40: em\_hg\_mus:\*

41: em\_hg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	5271	100.0	5271	6	BD237961	BD237961 Nucleic a
2	5271	100.0	5271	6	AR242771	AR242771 Sequence
3	5271	100.0	5300	6	AF007562	AF007562 Homo sapi
4	5271	100.0	6169	6	AR123665	AR123665 Sequence
5	5271	100.0	6169	6	BD237936	BD237936 Nucleic a
6	5271	100.0	6169	6	AR242746	AR242746 Sequence
7	5271	100.0	6169	6	BD065041	BD065041 Methods f
8	5246.4	99.5	5299	6	BD065039	BD065039 Methods f
9	5246.4	99.5	5300	6	AR123663	AR123663 Sequence
10	5246.4	99.5	5300	6	BD237934	BD237934 Nucleic a
11	5246.4	99.5	5300	6	AR242744	AR242744 Sequence
12	5232.4	99.3	79376	9	HS454G6	398750 Human DNA s
13	5224.4	99.1	5304	6	AR123664	AR123664 Sequence
14	5224.4	99.1	5304	6	BD237935	BD237935 Nucleic a
15	5224.4	99.1	5304	6	AR242745	AR242745 Sequence
16	5224.4	99.1	5304	6	BD065040	BD065040 Methods f
17	5181.4	98.3	170425	2	AC024490	AC024490 Homo sapi
18	1804.4	34.2	2800	6	AR212944	AR212944 Sequence
19	1804.4	34.2	2800	6	BD225246	BD225246 Remedies
20	1804.4	34.2	2800	9	HSMYOC1	AF049791 Homo sapi
21	432.6	8.2	1311	9	AY19012861	AY190128 Macaca fa
22	394.4	7.5	476	6	BD103416	BD103416 Gene rela
23	394.4	7.5	476	6	BD176938	BD176938 Gene rela
24	394.4	7.5	1086	9	HSGLCRA1	297171 Homo sapien
25	394.4	7.5	1228	9	AS0068651	AS006866 Homo sapi
26	227	4.3	227	6	BD237965	BD237965 Nucleic a
27	227	4.3	227	6	AR242775	AR242775 Sequence
28	227	4.3	283	6	BD237964	BD237964 Nucleic a
29	227	4.3	283	6	AR242774	AR242774 Sequence
30	219.4	4.2	182358	2	AC138218	AC138218 Mus muscu
31	211	4.0	23704	10	AF289236	AF289236 Mus muscu
32	194.6	3.7	160392	9	AC104236	AC104236 Homo sapi
33	191.8	3.6	246327	2	AC097054	AC097054 Rattus no
34	191.8	3.6	249765	2	AC129855	AC129855 Rattus no
35	190.8	3.6	16525	10	AF289235	AF289235 Rattus no
36	189.8	3.6	161577	9	AC007688	AC007688 Homo sapi
37	189	3.6	175627	9	AC107905	AC107905 Homo sapi
38	189	3.6	198857	9	AC012404	AC012404 Homo sapi
39	187.8	3.6	97037	9	AC004573	AC004573 Homo sapi
40	187.8	3.6	135038	9	HMMXMD703	L78810 Homo sapien
41	187.8	3.6	90906	9	AC079767	AC079767 Homo sapi
42	187.6	3.6	193267	2	AC009409	AC009409 Homo sapi
43	187.4	3.6	139776	9	AL160165	AL160165 Human DNA
44	185.8	3.5	1001	11	G73164	G73164 GL3-2 Human
45	185.8	3.5	76727	9	HS821D11	AL021453 Human DNA

## ALIGNMENTS

RESULT 1  
BD237961  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BD237961.  
Nucleic acids, kits, and methods for the diagnosis, prognosis and  
treatment of glaucoma and related disorders.  
BD237961.1 GI:33047731  
JP 2002534135-A/28.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 5271)  
Nucleic acids, kits, and methods for the diagnosis, prognosis and

Treatment of Glaucoma and related disorders  
Patent: JP 2002534135-A 28 15-OCT-2002;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
OS Homo sapiens (human)

PC 11-004N-1999 US 03/227881, 07-MAY-1999 US 09/306828 PI  
THAI D NGUYEN, JON R POLANSKY, PU CHEN, HUA CHEN PC  
C12N15/09, A61K31/573, A61K45/00, A61E27/06, C12N1/15, C12N1/19, PC  
C12N1/21,  
PC C12N5/10, C12N1/68, G01N33/53, G01N33/566, C12N5/00, C12N5/00 C0  
Nucleic acids, kits, and methods for the diagnosis, prognosis CC  
and

FEATURES	source
CC	treatment of glaucoma and related disorders
PH	Key
FT	Location/Qualifiers
FT	1. .5271
	/organisms='Homo sapiens (human)'
	Location/Qualifiers
	1. .5271

ORIGIN

Query Match	100.0%	Score 5271	DB 6	Length 5271
Best Local Similarity	100.0%	Prod. No. 0		
Matches 5271	Conservative . 0	Mismatches	0	Indels 0
		Gaps	0	

QY	1	ATCTTGTTCAGTTTAACCTCAGGGGCTATTGAATAAATAGATTAACAATGTGAAAG	60
Ddb	1	ATCTTGTTCAGTTTAACCTCAGGGGCTATTGAATAAATAGATTAACAATGTGAAAG	60
QY	61	TCTATTAACTGTATAGCTCCATTCGGATGTATGTCCTTGCGAGGATGATTAAGAATCA	120
Ddb	61	TCTATTAACTGTATAGCTCCATTCGGATGTATGTCCTTGCGAGGATGATTAAGAATCA	120
QY	121	GGAAGAAGAGTAGTACAGGTTAGGCCAAGTGCACAGGCTGTGTCTGCTTATTTTACTGA	180
Ddb	121	GGAAGAAGAGTAGTACAGGTTAGGCCAAGTGCACAGGCTGTGTCTGCTTATTTAGTGA	180
QY	181	CAGATGTGTGCTCTGACAGAAAGCTATTCTTCAGAAAATCATCATCCAAATGTGTAATC	240
Ddb	181	CAGATGTGTGCTCTGACAGAAAGCTATTCTTCAGAAAATCATCATCCAAATGTGTAATC	240
QY	241	CATCAAACAGAGCTTAAGAAAACAGAAATGATGGGCACTTCCCAAGAAAAATGCGAG	300
Ddb	241	CATCAAACAGAGCTTAAGAAAACAGAAATGATGGGCACTTCCCAAGAAAAATGCGAG	300
QY	301	GAGAGCAATTAATGATGAAAAATAAATTTTCCCTTGTTTTAATTCAGAAAAAATG	360
Ddb	301	GAGAGCAATTAATGATGAAAAATAAATTTTCCCTTGTTTTAATTCAGAAAAAATG	360
QY	361	ATGAGGACCAAAATCATGATAATANGAAAAACAGCTCAGAAAAAAGATTTCMAATTGG	420
Ddb	361	ATGAGGACCAAAATCATGATAATANGAAAAACAGCTCAGAAAAAAGATTTCMAATTGG	420
QY	421	TATTTAGTATTTGTTCTTGGAAGAGAACCTCATGTAGCTTGATGGGAAAAATGGAA	480
Ddb	421	TATTTAGTATTTGTTCTTGGAAGAGAACCTCATGTAGCTTGATGGGAAAAATGGAA	480
QY	481	AAACGTCAAAAGCATGATGTATCAAGTCCCAAAGTGGATTATTTATTTAAAAACAGAT	540
Ddb	481	AAACGTCAAAAGCATGATGTATCAAGTCCCAAAGTGGATTATTTATTTAAAAACAGAT	540
QY	541	GGCATCACTCTGGGAGAGCAAGTTCAGAAAGGTCATGTTACAAAGACATTAACATTAAC	600
Ddb	541	GGCATCACTCTGGGAGAGCAAGTTCAGAAAGGTCATGTTACAAAGACATTAACATTAAC	600
QY	601	AGCAAAATCAAAATTCGCAAAATGCAAGAGAAAAATGGGACTGGGAACCTTTCATAC	660
Ddb	601	AGCAAAATCAAAATTCGCGAAATGCAAGAGAAAAATGGGACTGGGAACCTTTCATAC	660

QY	661	AGGATATGAGCACTGTGACCACTGTTGGCACAACCTCCCGCTCTATACAGGGAAACACAAA	720
Db	661	AGGATATGAGCACTGTGACCACTGTTGGCACAACCTCCCGCTCTATACAGGGAAACACAAA	720
QY	721	ATTGACTGGGCTTAAGCCTGGACTTTCAAGGAAATATGAAAACTAGAGCAAAACAAA	780
Db	721	ATTGACTGGGCTTAAGCCTGGACTTTCAAGGAAATATGAAAACTAGAGCAAAACAAA	780
QY	781	GACATGTTTAAAGGCAACCAACATTTGAGCCTTCAAGCAGCGTGCCCTTCAGCA	840
Db	781	GACATGTTTAAAGGCAACCAACATTTGAGCCTTCAAGCAGCGTGCCCTTCAGCA	840
QY	841	GGGACCCCTGAGGCAATTTGCTTTAGGAAAGCCAGTTTCTTAAGGAATCTTAAAGAACTC	900
Db	841	GGGACCCCTGAGGCAATTTGCTTTAGGAAAGCCAGTTTCTTAAGGAATCTTAAAGAACTC	900
QY	901	TTGAAAGATCATGAATTTTAAACCATTTTAAGTATAAACAAATATGCAATCATATCAG	960
Db	901	TTGAAAGATCATGAATTTTAAACCATTTTAAGTATAAACAAATATGCAATCATATCAG	960
QY	961	TTTAGACATGGGGTCCCAATTTTATTAAGTCAGGCAATACAGATTAAGTGCCCGCTCC	1020
Db	961	TTTAGACATGGGGTCCCAATTTTATTAAGTCAGGCAATACAGATTAAGTGCCCGCTCC	1020
QY	1021	GGATAGGTCAGAAATCATTAAGAAATCACTGTGTCCCAATCTTAATTTTTCAGATGATC	1080
Db	1021	GGATAGGTCAGAAATCATTAAGAAATCACTGTGTCCCAATCTTAATTTTTCAGATGATC	1080
QY	1081	TGTGCATAGCCCTCACACACAGGCCGGAATGTGTCTACCTATACACACACTTACACCCAA	1140
Db	1081	TGTGCATAGCCCTCACACACAGGCCGGAATGTGTCTACCTATACACACACTTACACCCAA	1140
QY	1141	GTGCTCAACCAATTTTAAACGTGATCTCAGTAGGTCCCAATTAACAAATGCACTGCC	1200
Db	1141	GTGCTCAACCAATTTTAAACGTGATCTCAGTAGGTCCCAATTAACAAATGCACTGCC	1200
QY	1201	TGTGAGGCCATCCCGCTCCACAGGAATCTCCCACTCTGACCTTCGATCAACATGT	1260
Db	1201	TGTGAGGCCATCCCGCTCCACAGGAATCTCCCACTCTGACCTTCGATCAACATGT	1260
QY	1261	TACAGCCAGAAAGCTCCGAGGGATGAGGTCTGTCTTCAACCTACCTGATGACTCTAC	1320
Db	1261	TACAGCCAGAAAGCTCCGAGGGATGAGGTCTGTCTTCAACCTACCTGATGACTCTAC	1320
QY	1321	ACCTGAGCTCACTGCAACCTCTGCTCCCAAGTTCAAGCAATTTCTGTCTACGCTCC	1380
Db	1321	ACCTGAGCTCACTGCAACCTCTGCTCCCAAGTTCAAGCAATTTCTGTCTACGCTCC	1380
QY	1381	CGCGTAGCTGGGACCTACAGGCGCACGCCCGGCTAATTTGTATGTATGATAGAGAGGG	1440
Db	1381	CGCGTAGCTGGGACCTACAGGCGCACGCCCGGCTAATTTGTATGTATGATAGAGAGGG	1440
QY	1441	GTTTCACCAATTTAGCCCGGCTGTGTTGAATCTGACCTCAGGTATCCACCACCTC	1500
Db	1441	GTTTCACCAATTTAGCCCGGCTGTGTTGAATCTGACCTCAGGTATCCACCACCTC	1500
QY	1501	AGCCCTCTAAAGTCTGCGGATTAAGGCAATGAGTCAACCGGCCCGGCAAGGCTCACTGT	1560
Db	1501	AGCCCTCTAAAGTCTGCGGATTAAGGCAATGAGTCAACCGGCCCGGCAAGGCTCACTGT	1560
QY	1561	TTAATTAAGATATCTTGAATGTTTCTTAACCAACAGGGAAACAGACAAAGCTGTGA	1620
Db	1561	TTAATTAAGATATCTTGAATGTTTCTTAACCAACAGGGAAACAGACAAAGCTGTGA	1620
QY	1621	TAAATTTAAGGATTTCTTGGATGGGGAATGTGTCATGAGCTGCTGCTTAGTCCAGAC	1680
Db	1621	TAAATTTAAGGATTTCTTGGATGGGGAATGTGTCATGAGCTGCTGCTTAGTCCAGAC	1680
QY	1681	CACGTGCTCTATCACTTTCTTCCCTCATCTCATTTTCAAGGCTAAGTTTATTTATTT	1740
Db	1681	CACGTGCTCTATCACTTTCTTCCCTCATCTCATTTTCAAGGCTAAGTTTATTTATTT	1740
QY	1741	CACCACTCTTTGTGTGTAAGCTCCACATCTGTATCTGAATAATAGATATATACATTAAC	1800

Db 1741 CACCAATGCTTTTGGTGAAGCTCCACATCGTTAATAAATGAAGATATACATAAATAAG 1800  
 Qy 1801 TTCCATTTGGGGCCACTGTGTGTGTGTATAGAGGAGAGGAGATACCCAGAGACTCT 1860  
 Db 1801 TTCCATTTGGGGCCACTGTGTGTGTGTATAGAGGAGAGGAGATACCCAGAGACTCT 1860  
 Qy 1861 TGAAGCCCCCGGAGAGGATTTCTCTCTCAAGCTGGGGAGAGCCCTGCAAGACCCGGGCTC 1920  
 Db 1861 TGAAGCCCCCGGAGAGGATTTCTCTCTCAAGCTGGGGAGAGCCCTGCAAGACCCGGGCTC 1920  
 Qy 1921 TGGGTGCTGTAGCAACTGCGACCCGCTGCACTGCTGTTTGTATCACTCTAG 1980  
 Db 1921 TGGGTGCTGTAGCAACTGCGACCCGCTGCACTGCTGTTTGTATCACTCTAG 1980  
 Qy 1981 GACCTGTGCTTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
 Db 1981 GACCTGTGCTTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
 Qy 2041 TATTGAGTACTTATATCTGCGACACCAAGACAAATGATGAGCAAAAGAGCTGCTG 2100  
 Db 2041 TATTGAGTACTTATATCTGCGACACCAAGACAAATGATGAGCAAAAGAGCTGCTG 2100  
 Qy 2101 CCTACCTTGTGTAGAGTGAAGTTTCTCATGAGAGCTGCAAGAGAAATTAATGCA 2160  
 Db 2101 CCTACCTTGTGTAGAGTGAAGTTTCTCATGAGAGCTGCAAGAGAAATTAATGCA 2160  
 Qy 2161 GCGAATTAACCCAGTCTGAAGAAAGAAATTAACCATCTTGAAGAAATGAGG 2220  
 Db 2161 GCGAATTAACCCAGTCTGAAGAAAGAAATTAACCATCTTGAAGAAATGAGG 2220  
 Qy 2221 AGCATCTCTTAACAAAGCCACCTCTAGGCCCCCTGCTGCTCATGCTGCTGCTGCTG 2280  
 Db 2221 AGCATCTCTTAACAAAGCCACCTCTAGGCCCCCTGCTGCTCATGCTGCTGCTGCTG 2280  
 Qy 2281 CCCCCAAGCCGAGTCTTCCAAAGCTCTCTCCATCATGCTGCTGCTGCTGCTGCTGCTG 2340  
 Db 2281 CCCCCAAGCCGAGTCTTCCAAAGCTCTCTCCATCATGCTGCTGCTGCTGCTGCTGCTG 2340  
 Qy 2341 GCTGTGCTTCCGCTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400  
 Db 2341 GCTGTGCTTCCGCTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400  
 Qy 2401 CAGAAAGAAATGAGAGGAGAACTAGTCTAAGGAGATCTGAGGGAGACAGTCTT 2460  
 Db 2401 CAGAAAGAAATGAGAGGAGAACTAGTCTAAGGAGATCTGAGGGAGACAGTCTT 2460  
 Qy 2461 CTCAGAGGAGAGGAGCTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTGCAAGAG 2520  
 Db 2461 CTCAGAGGAGAGGAGCTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTGCAAGAG 2520  
 Qy 2521 TGGGAGCGCTGGGCTGAGCGGCTGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 2580  
 Db 2521 TGGGAGCGCTGGGCTGAGCGGCTGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAG 2580  
 Qy 2581 GCTGCGAGATGTCAGTGTGTGTCAAGGAGCTGGAGATTTTCCGTTGCTTCTGAGC 2640  
 Db 2581 GCTGCGAGATGTCAGTGTGTGTCAAGGAGCTGGAGATTTTCCGTTGCTTCTGAGC 2640  
 Qy 2641 CTTTATCTTTTCTGCTGCTGAGAGAGAGAGATTAATTCATGAGAGAGAGAGAGAGTTC 2700  
 Db 2641 CTTTATCTTTTCTGCTGCTGAGAGAGAGAGATTAATTCATGAGAGAGAGAGAGTTC 2700  
 Qy 2701 AATAAGTCACTGTTAAATTCAGAGGCTGAGTGTGCTTCTTCAAGAGCTTAT 2760  
 Db 2701 AATAAGTCACTGTTAAATTCAGAGGCTGAGTGTGCTTCTTCAAGAGCTTAT 2760  
 Qy 2761 TTAATGGGAATATAGAGAGAGCTATTCCTAGGCTTAAATTCAGAGAGAGAGAGAGTAC 2820  
 Db 2761 TTAATGGGAATATAGAGAGAGCTATTCCTAGGCTTAAATTCAGAGAGAGAGAGTAC 2820  
 Qy 2821 TGGAGCTTTTCTTCTGATGTCTTCTGAGCACTACTACGCTGCTGAGTGTGCTTGA 2880

Db 2881 TGGAGCTTTTCTTCTGATGTCTTCTGAGCACTACTACGCTGCTGAGCTTGA 2880  
 Qy 2881 TGGAGCTTTTCTTCTGATGTCTTCTGAGCACTACTACTAGACTGCTGATTTCTTCTGAGCTTGA 2940  
 Db 2881 TGGAGCTTTTCTTCTGATGTCTTCTGAGCACTACTACTAGACTGCTGATTTCTTCTGAGCTTGA 2940  
 Qy 2941 GGTGGCTGTGAGAGCTGAGAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3000  
 Db 2941 GGTGGCTGTGAGAGCTGAGAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3000  
 Qy 3001 AATAAGCTTTGAGCTCTGATGTCTGAGCACTTCTCTGATGTCTGAGAGG 3060  
 Db 3001 AATAAGCTTTGAGCTCTGATGTGTGTGAGCACTTCTCTGATGTCTGAGAGG 3060  
 Qy 3061 GATTTGAG 3120  
 Db 3061 GATTTGAG 3120  
 Qy 3121 GAG 3180  
 Db 3121 GAG 3180  
 Qy 3181 CAG 3240  
 Db 3181 CAG 3240  
 Qy 3241 TCCCTAG 3300  
 Db 3241 TCCCTAG 3300  
 Qy 3301 GGTAGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360  
 Db 3301 GGTAGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360  
 Qy 3361 TTAACCTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420  
 Db 3361 TTAACCTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420  
 Qy 3421 AGTGAAGCTTCAAG 3480  
 Db 3421 AGTGAAGCTTCAAG 3480  
 Qy 3481 ACAGATTCATTAAG 3540  
 Db 3481 ACAGATTCATTAAG 3540  
 Qy 3541 GTTCTGAG 3600  
 Db 3541 GTTCTGAG 3600  
 Qy 3601 CCGATTTCTAATTAATTAATTTTCTTCAAGCTGATTAATCTGAGAGAGAGAGAGAGAGAG 3660  
 Db 3601 CCGATTTCTAATTAATTAATTTTCTTCAAGCTGATTAATCTGAGAGAGAGAGAGAGAGAG 3660  
 Qy 3661 GTAGTACTGAGAGCTGTAAGATTAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3720  
 Db 3661 GTAGTACTGAGAGCTGTAAGATTAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3720  
 Qy 3721 GAGGTAG 3780  
 Db 3721 GAGGTAG 3780  
 Qy 3781 TAAAGCCTAAG 3840  
 Db 3781 TAAAGCCTAAG 3840  
 Qy 3841 CATTTAG 3900  
 Db 3841 CATTTAG 3900  
 Qy 3901 TAAACCAACCAAG 3960  
 Db 3901 TAAACCAACCAAG 3960

QY 3961 AGAATAGATCTTTAGAGCAAACTGTTTCTCCACATCGAGTGAAGTCTGCCAGGCG 4020
Db 3961 AGAATAGATCTTTAGAGCAAACTGTTTCTCCACATCGAGTGAAGTCTGCCAGGCG 4020
QY 4021 AGTTGGAAATATTTACTCTCACAGTATTTGACACTGTGTGGTATTTAAACAATTAAGT 4080
Db 4021 AGTTGGAAATATTTACTCTCACAGTATTTGACACTGTGTGGTATTTAAACAATTAAGT 4080
QY 4081 TGCTCAAGGCAATCATTTATTTCAAGTGGTAAAGTACTCTTGACAGTCTTTGGTAAAT 4140
Db 4081 TGCTCAAGGCAATCATTTATTTCAAGTGGTAAAGTACTCTTGACAGTCTTTGGTAAAT 4140
QY 4141 TTATGGCTATTTGGCAATTTGGCTTTTGTGTTTCTCTTTGGGTTTATTAATGTAAGCAG 4200
Db 4141 TTATGGCTATTTGGCAATTTGGCTTTTGTGTTTCTCTTTGGGTTTATTAATGTAAGCAG 4200
QY 4201 GGATTTATTAACCTACAGTCCAGAAAGCCGTGTAATTTGATAGAGAAATTTACATTTT 4260
Db 4201 GGATTTATTAACCTACAGTCCAGAAAGCCGTGTAATTTGATAGAGAAATTTACATTTT 4260
QY 4261 TGTTTTTACCACTCTTCTACATTAATTTAAACATTTTATTCATTGGCAATAGAGCCATTA 4320
Db 4261 TGTTTTTACCACTCTTCTACATTAATTTAAACATTTTATTCATTGGCAATAGAGCCATTA 4320
QY 4321 CTCAAGTGTGTATTAACAGTACCTGTGATTTGTGCTATTTCCAAATGAATTCACAGACATT 4380
Db 4321 CTCAAGTGTGTATTAACAGTACCTGTGATTTGTGCTATTTCCAAATGAATTCACAGACATT 4380
QY 4381 TTATACTATATTAACAGTGTGTGCAATACCTGTGTAAGTAAATATTTTACTCAAACTA 4440
Db 4381 TTATACTATATTAACAGTGTGTGCAATACCTGTGTAAGTAAATATTTTACTCAAACTA 4440
QY 4441 CTTTGAATATAGACCTCCCTGCTGAGTCTTGTGTTTAAATTAATTAACATGTTTAA 4500
Db 4441 CTTTGAATATAGACCTCCCTGCTGAGTCTTGTGTTTAAATTAATTAACATGTTTAA 4500
QY 4501 ATTTGATATTTGATATATCATTTTCAATTTGATTTGCTTGTGATCTATATTTT 4560
Db 4501 ATTTGATATTTGATATATCATTTTCAATTTGATTTGCTTGTGATCTATATTTT 4560
QY 4561 ATATATTTGAAACATCTTTCTGAGAGAGTCTCCCAAGTTTCAACATGAGTCTTGG 4620
Db 4561 ATATATTTGAAACATCTTTCTGAGAGAGTCTCCCAAGTTTCAACATGAGTCTTGG 4620
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LOCUS AR242771
DEFINITION Sequence 34 from patent US 6475724.
ACCESSION AR242771
VERSION AR242771.1 GI:27289410
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5271)
AUTHORS Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
TITLE Nucleic acids, kits, and methods for the diagnosis, prognosis and
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/organism="unknown"
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Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and Polansky,U.R.  
 TITLE Gene structure and properties of TIGR, an olfactomedin-related glycoprotein cloned from glucocorticoid-induced trabecular meshwork cells

JOURNAL J. Biol. Chem. 273 (11), 6341-6350 (1998)  
 MEDLINE 98165818  
 PUBMED 9497363  
 REFERENCE 2 (bases 1 to 5300)  
 AUTHORS Nguyen,T.D., Chen,P., Chen,H. and Polansky,U.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-JUN-1997) Ophthalmology, University of California San Francisco, 10 Kirkham Street, San Francisco, CA 94143-0730, USA

FEATURES  
 source location/Qualifiers

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VERSION ARI23665.1 GI:14109026  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 6169)  
AUTHORS Nguyen T.D., Polansky, J.R., Chen, P. and Chen, H.  
TITLE Methods for the diagnosis, prognosis and treatment of gliucoma and related disorders  
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RESULT 5
LOCUS BD237936
DEFINITION Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders.
ACCESSION BD237936
VERSION BD237936.1
KEYWORDS JP 2002534135-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6169)
AUTHORS Nguyen,T.D., Polansky,V.R., Chen,P. and Chen,H.
TITLE Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders
JOURNAL Patent: JP 2002534135-A 3 15-OCT-2002; THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT OS Homo sapiens (human)
PN JP 2002534135-A/3
PD 15-OCT-2002
PF 11-JAN-2000 JP 2000593777
PR 11-JAN-1999 US 09/227881,07-MAY-1999 US 09/306828 PI
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C12N1/5/09,A61K31/573,A61K45/00,A61P27/06,C12N1/15,C12N1/19, PC
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PC C12N5/10,C12Q1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC
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 ACCESSION BD065039  
 VERSION BD065039.1 GI:22610642  
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 SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE 1 (bases 1 to 5299)  
 AUTHORS Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.  
 TITLE Methods for the diagnosis, prognosis and treatment of glaucoma and related disorders  
 JOURNAL Patent: JP 2001509669-A 1 24-JUL-2001;  
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 COMMENT OS Unidentified  
 PN JP 2001509669-A/1  
 PD 24-JUL-2001  
 PF 09-JAN-1998 JP 1998532017  
 PR 28-JAN-1997 US 08/791154,26-SEP-1997 US 08/938669 P1  
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 AUTHORS Nuyven, T.D., Polansky, J.R., Chen, P. and Chen, H.  
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Nucleic acids, kits, and methods for the diagnosis, prognosis
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QY	121	GGAAGAAGAGATACCAAGTTAGCCAAATGTCCAGCGCTGTGTCTGCTTATTTTAGTA	180	
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QY	4200	GGGATTTATTAACCTTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTAATTT	4259
Db	4200	GGGATTTATTAACCTTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTTACATTT	42599
QY	4260	TTGTTTTTACACCTTCTACTTAATTTAATATTTTTCATTTGGGAATTAAGGCATTA	4319
Db	4260	TTGTTTTTACACCTTCTACTTAATTTAATATTTTATTCATTGGGAATTAAGGCATTA	43199
QY	4320	ACTCAAGTGTAAATTAACAGTACCTGTGATTTTGTCAATTCGAATGAATCACAGACAT	4379
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QY	4380	TTTATCTATTAATACGTTTGTGCAATACGTTGTAAATTAATTTTACTCAAACT	4439
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QY	4440	ACTTTGAAATTAAGACCTCCTGTGTGATCTGTTTTTACATATTAATAAATCATGTTAA	4499
Db	4440	ACTTTGAAATTAAGACCTCCTGTGTGATCTGTTTTTACATATTAATAAATCATGTTAA	44999
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QY	4560	TATATATTTGAAACATCTTCTGTGAAGAAGTCCCAAGTTTCCCAATGAGGTTCTTG	4619
Db	4560	TATATATTTGAAACATCTTCTGTGAAGAAGTCCCAAGTTTCCCAATGAGGTTCTTG	46199
QY	4620	GCATGACACACACAGAGTAAGAAGTGAATTAAGGCTTAACATGACATGTGTGCTGAG	4679
Db	4620	GCATGACACACACAGAGTAAGAAGTGAATTAAGGCTTAACATGACATGTGTGCTGAG	46799
QY	4680	ATGCAAGATGAAATTAAGAAATCTCCCAAGATACACAGTGTTTTAAAGCTAGGGGT	4739
Db	4680	ATGCAAGATGAAATTAAGAAATCTCCCAAGATACACAGTGTTTTAAAGCTAGGGGT	47399
QY	4740	GAGGGGGGAAATCTGCGCCTTCATTAAGAAATGCTTCTCCGAGCCTGTAGGGTCTGT	4799
Db	4740	GAGGGGGGAAATCTGCGCCTTCATTAAGAAATGCTTCTCCGAGCCTGTAGGGTCTGT	47999
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QY	4860	TGGAATCTCAATTCCTAGCAATAGTGCTGGACAGTGCAGGTTTCTCAATGAATTTGACA	4919
Db	4860	TGGAATCTCAATTCCTAGCAATAGTGCTGGACAGTGCAGGTTTCTCAATGAATTTGACA	49199
QY	4920	GTTGAATGAAAAATTAACATAGAAATATATCTTGTGAATCAGACACACAGTATGCTGT	4979
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QY	4980	GTTGAATGTTGTGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAACACAGTGAAT	5039
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QY	5040	ATAGGAACATTAATTTGGGGGTAATGGGTCATAAATGGGATGTTCTTTTAAAGAAACT	5099
Db	5040	ATAGGAACATTAATTTGGGGGTAATGGGTCATAAATGGGATGTTCTTTTAAAGAAACT	50999

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Db		5160	CCCTGTGCACAGCCCCACCGCCCTCACGTCACACCTCTGTCTTCCCOCATGAAGGCT	5219
QY		5220	GGCTTCCCAAGTATATATAAACCTCTCTGGAGCTGTGGGATGAGCCACAGAG	5271
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AR242744				
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DEFINITION		Sequence 1 from patent US 6475724.		
ACCESSION		AR242744		
VERSION		AR242744.1	GI:27289383	
KEYWORDS				
SOURCE		Unknown.		
ORGANISM		Unknown.		
REFERENCE		Unclassified.		
AUTHORS		1 (bases 1 to 5300)		
TITLE		Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H. Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders Patent: US 6475724-A 1 05-NOV-2002;		
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			/mol_type="genomic DNA"	
ORIGIN				
Query Match		99.5%; Score 5246.4; DB 6; Length 5300;		
Best Local Similarity		99.9%; Pred. No. 0;		
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Db		1	ATCTTTGTCAGTTTAACCTCAGGGCTATTATGAATGAATGAGATTAACCATGTGAAG	60
QY		61	TCCATATAACTGTATACCTCCCATTTGGAGTATGTCTTTGGCAGATGATAAGAATCA	120
Db		61	TCCATATAACTGTATACCTCCCATTTGGAGTATGTCTTTGGCAGATGATAAGAATCA	120
QY		121	GGAAGAAGAGATCACGTTAGCCAAAGTCCAGGCTGTGTCTGCTCTATTATTAGTGA	180
Db		121	GGAAGAAGAGATCACGTTAGCCAAAGTCCAGGCTGTGTCTGCTCTATTATTAGTGA	180
QY		181	CAGATGTTGCTCTGCACAGAAAGCTATTCTTCAGAAAATCATCATCATATATGTAAATC	240
Db		181	CAGATGTTGCTCTGCACAGAAAGCTATTCTTCAGAAAATCATCATCATATATGTAAATC	240
QY		241	CATATAACAGAGGTAGAAGACAGGAATGAGTGGGCACTTGCCCAAGAAAAATCCAG	300
Db		241	CATATAACAGAGGTAGAAGACAGGAATGAGTGGGCACTTGCCCAAGAAAAATCCAG	300
QY		301	GAGAGCAAATPATGATGAAAAATPAACTTTCCCTTTGTTTTTAATTTCAGAAAAAATG	360
Db		301	GAGAGCAAATPATGATGAAAAATPAACTTTCCCTTTGTTTTTAATTTCAGAAAAAATG	360
QY		361	ATGAGGACCAATPATGATGATAAGAAAAACAGCTAGAAAAAAGATGTTTCCAATTGG	420
Db		361	ATGAGGACCAATPATGATGATAAGAAAAACAGCTAGAAAAAAGATGTTTCCAATTGG	420
QY		421	TAAATTAGTATTTTGTTCTTGGGAAAGACCTTCATGTAGTGTGATGGGAAATGGAA	480
Db		421	TAAATTAGTATTTTGTTCTTGGGAAAGACCTTCATGTAGTGTGATGGGAAATGGAA	480
QY		481	AAAGGTCAAAAGCATATCTGCATCAATGCCAAAGTGATATTAATTTPAAAAACAGAT	540
Db		481	AAAGGTCAAAAGCATATCTGCATCAATGCCAAAGTGATATTAATTTPAAAAACAGAT	540

QY	541	GGCATCACTCTGGGGAGGCAAGTTCAGGAAGTCATGTTAGCAAAAGACATTAACAATAAC	600
Db	541	GGCATCACTCTGGGGAGGCAAGTTCAGGAAGTCATGTTAGCAAAAGACATTAACAATAAC	600
QY	601	AGCAAAATCAAAATTCGCGCAATGCAAGAGAGAAAATGGGGACTGGGAAAGCTTCAATAAC	660
Db	601	AGCAAAATCAAAATTCGCGCAATGCAAGAGAGAAAATGGGGACTGGGAAAGCTTCAATAAC	660
QY	661	AGGATTAAGGCAAGTGAACAAGTTCGCAACACCTCCCGCTCTATCAAGAGGACACAAAA	720
Db	661	AGGATTAAGGCAAGTGAACAAGTTCGCAACACCTCCCGCTCTATCAAGAGGACACAAAA	720
QY	721	ATTGACTGGGCTAAGCCTGGACTTTTCAAGGGAAATATGAAAACTGAGACCAAAACAAA	780
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QY	781	GACATGGTTAAAGGCAACGAGACATTTGGAGGCTTCAAGGACAGAGTCCCTCAGCA	840
Db	781	GACATGGTTAAAGGCAACGAGACATTTGGAGGCTTCAAGGACAGAGTCCCTCAGCA	840
QY	841	GGACCCCTGAGGCAATTTGCTTTAGGAAGCAGTTTTCTTAAGGAATCTTAAGAAATC	900
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QY	901	TTGAAAGATCATGAATTTTAACCATTTTAAGTATMAAACAAATATGGGATGCAATATCAG	960
Db	901	TTGAAAGATCATGAATTTTAACCATTTTAAGTATMAAACAAATATGGGATGCAATATCAG	960
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Db	961	TTTGAACATGGGTCGCCAATTTTAAATAGTCAGGATCAAGAGATTAAGTCCAGCTCC	1020
QY	1021	GGATTAAGTCAGAAAATCATTTAGAAATCACTGTGTCCCATCTTAATCTTTTCAGATATC	1080
Db	1021	GGATTAAGTCAGAAAATCATTTAGAAATCACTGTGTCCCATCTTAATCTTTTCAGATATC	1080
QY	1081	TGTCATAGCCTTCACACACAGGCCGAGTGTGACCTCAACACATCATCAACCCAA	1140
Db	1081	TGTCATAGCCTTCACACACAGGCCGAGTGTGACCTCAACACATCATCAACCCAA	1140
QY	1141	GTCGCTCAACCATTTGTAACGTGTCATCTCAGTAGTGTCCATTACAAATGCGACCTCCC	1200
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QY	1201	TGTGAGCCCATCCGCTTCACAGGAATCTCCCATCTGAGACTTCGCAATCAGATGT	1260
Db	1201	TGTGAGCCCATCCGCTTCACAGGAATCTCCCATCTGAGACTTCGCAATCAGATGT	1260
QY	1261	TACAGCCAGAAAGCTCCGTGAGGGGTAGGGTCTGTGTCTTAACACTACTGTATGCTTAC	1320
Db	1261	TACAGCCAGAAAGCTCCGTGAGGGGTAGGGTCTGTGTCTTAACACTACTGTATGCTTAC	1320
QY	1321	ACCTGAGCTCACTGCAACCTGTGCTCCCGAGTTCAGGAATTTCTCTGTCTCAGCTCC	1380
Db	1321	ACCTGAGCTCACTGCAACCTGTGCTCCCGAGTTCAGGAATTTCTCTGTCTCAGCTCC	1380
QY	1381	CGCGTAGCTGGGACATACAGGGGCAAGCCGCGTAAATTTTGTGATATGTTAGTAGATGGG	1440
Db	1381	CGCGTAGCTGGGACATACAGGGGCAAGCCGCGTAAATTTTGTGATATGTTAGTAGATGGG	1440
QY	1441	GTTTCAACCATATTAGCCGCGTGTCTTGAACTCTCTGACTCAGGTGATCCACCACTC	1500
Db	1441	GTTTCAACCATATTAGCCGCGTGTCTTGAACTCTCTGACTCAGGTGATCCACCACTC	1500
QY	1501	AGCCTCTTAAAGTCTGGGATTTACAGGCAATGATCAACCGCGCCGGCAAGGGTCAAGGT	1560
Db	1501	AGCCTCTTAAAGTCTGGGATTTACAGGCAATGATCAACCGCGCCGGCAAGGGTCAAGGT	1560
QY	1561	TTTAAATAGGAATTAATCTGTAATGGTTTAACTAAACCAACAGGGAACAGACAAAAGCTGTGA	1620
Db	1561	TTTAAATAGGAATTAATCTGTAATGGTTTAACTAAACCAACAGGGAACAGACAAAAGCTGTGA	1620

QY	1621	TAATTTACAGGGATTTCTTGGAATGGGGAAATGGTGCATAGAGCTCCGCTACAGCCAGAC	1680
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QY	1681	CACGTGCTCCATCACTTTCTTCCTCCATCCTCATTTTCAAGCTAATTAACATTTAT	1740
Db	1681	CACGTGCTCCATCACTTTCTTCCTCCATCCTCATTTTCAAGCTAATTAACATTTAT	1740
QY	1741	CACCATGCTTTTGTGTGAACCTTCCACATGCTTACAGAAATAGAGTATACATAAACTAG	1800
Db	1741	CACCATGCTTTTGTGTGAACCTTCCACATGCTTACAGAAATAGAGTATACATAAACTAG	1800
QY	1801	TTTCATTTGGGGCATCTGTGTGTGTGTATAGGGGAGAGAGGCATACCCAGAGCTCT	1860
Db	1801	TTTCATTTGGGGCATCTGTGTGTGTGTATAGGGGAGAGAGGCATACCCAGAGCTCT	1860
QY	1861	TGAAGCCCCCGGAGAGGTTTCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCC	1920
Db	1861	TGAAGCCCCCGGAGAGGTTTCTCTCCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCC	1920
QY	1921	TGGGTGTCCTGAGAACCTGCAAGCCCGTCCACTGGTTGTTTGTATCACTCTCTAG	1980
Db	1921	TGGGTGTCCTGAGAACCTGCAAGCCCGTCCACTGGTTGTTTGTATCACTCTCTAG	1980
QY	1981	GACCTGTGCTTTCTATTTCTGTGTGAATCGTTTCATTCACAGCATTCATTGACAT	2040
Db	1981	GACCTGTGCTTTCTATTTCTGTGTGAATCGTTTCATTCACAGCATTCATTGACAT	2040
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Db	2041	TATTGAGTACTTATATCTGCGACACACACAGACAAATGGTAGAGCAACAGCACTGC	2100
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Db	2101	CTACACCTCGTGAAGGTACAGTTTCTCATGAGAGAGTGCAGAGAAAATTAATAGCA	2160
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QY	2221	AGCATCCCTTAAACAAGGCACCTCCAGAGCCCCCGTCTCCATTCGAGCCGAGG	2280
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QY	2281	CCCCCAGCCGAGTCTTCAAGCTCTCTCTCATCATGTCACAGCGCTCAGCTGCGCT	2340
Db	2281	CCCCCAGCCGAGTCTTCAAGCTCTCTCTCATCATGTCACAGCGCTCAGCTGCGCT	2340
QY	2341	GCTTGCTTCCCGTGAATGTCGTCGTGTGSCATCTAGCTGAGACCTCTTGCTCAAGCT	2400
Db	2341	GCTTGCTTCCCGTGAATGTCGTCGTGTGSCATCTAGCTGAGACCTCTTGCTCAAGCT	2400
QY	2401	CCAGAAAGAAATGAGAGAGGAACTAGTCTTACAGAGAAATCTGAGAGGACAGTGTTC	2460
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QY	2461	CTCAGAGGAAAGGGGCTCCACGTCCAGAGAAATTCAGAGAGTGGGACATGCAAGGAG	2520
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QY	2521	TGGGGACGCTGGGGCTGAGACGGGTCTCAAAAGGACAGAGGTGAAGAAAGGCAAGCTGAA	2580
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QY	2581	GCTGCCAGATTTCAGTGTTTCAAGGGGCTGGAGTTTCCGTGCTTCTGTGAGC	2640
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Qy 3301 GGTAGCTTTTGGCTGGCATTTCAAAAATGGGCCAGAGCAAGTGAATGCGCAGAGTTG 3360
Db 3301 GGTAGCTTTTGGCTGGCATTTCAAAAATGGGCCAGAGCAAGTGAATGCGCAGAGTTG 3360
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Db 4200 GGAATTTTAACTTCACTCCAGAAAGCTGTGAATTTGAATGAGAAAATTTACATTT 4259
Qy 4260 TTGTTTATTAACACTTCACTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTT 4319
Db 4260 TTGTTTATTAACACTTCACTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTT 4319
Qy 4320 ACTCAAGTGGTATTAAGTACAGTGTGATTTGTCAATTACCAATGAAATCAAGACAT 4379
Db 4320 ACTCAAGTGGTATTAAGTACAGTGTGATTTGTCAATTACCAATGAAATCAAGACAT 4379
Qy 4380 TTTATTAATTTAAGTGTGAGATGTTGAGATGCTTGAATGAGGAGGAGGAGGAGGAG 4439
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[illegible]

RESULT 12	HS454G6/c	LOCUS	DEFINITION
HS454G6	79376 bp	DNA	linear
Human DNA sequence from clone RPJ-454G6 on chromosome 1q24, complete sequence.			

ACCESSION	Z98750
VERSION	Z98750.1
KEYWORDS	GI:2887277
SOURCE	HTG.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
JOURNAL	1 (bases 1 to 79376)
COMMENT	Pavitt, R. Direct Submission Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humgery@sanger.ac.uk On Feb 14, 1998 this sequence version replaced gi:2465060.

Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk)

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate strand. Regions that were not sequenced were indicated by a dash (-). Chemistry or covered by high quality data (i.e., phred quality > 30). An attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wg; WORMPEP; Information on the WORMPEP database can be found at <http://www.wormbase.org>.

was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at [http://www.sanger.ac.uk/projects/c\\_elegans/wormmap](http://www.sanger.ac.uk/projects/c_elegans/wormmap) this sequence

<http://www.sanger.ac.uk/HGP/Ch1.RP3-454G6> is from the library PCOI-3 constructed by the group of  
 pleier de Jong. For further details see  
<http://www.choiri.org/bacpac/home.htm>  
 VECTOR: pCYPAC2  
 IMPORTANT: This sequence is not the entire insert of clone  
 RP3-454G6 It may be shorter because we sequence overlapping  
 sections only once, except for a short overlap.  
 The true left end of clone RP3-454G6 is at 1 in this sequence. The  
 true left end of clone RP4-560B9 is at 79273 in this sequence.  
 Location/Qualifiers  
 1..79376

gene	complement(46386..63072) /gene="MYOC"
mRNA	complement(join(46386..47170,49058..49183,62469..63072) /cdo="MYOC")

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CDS
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/product="d44546.1 (myocilin, trabecular meshwork inducible glucocorticoid response (TIGR))"
/evidence=not experimental
complement(join(45386..47170,49058..49183,62465..63030))

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Query Match	99.3%	Score 5232.4;	DB 9;	Length 79376;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 5267;	Conservative	0;	Mismatches 1;	Indels 4; Gaps 3;

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Qy	61	TCCCTAAACCTGTATAGCCTCCATTCGGAATGATGTGTTCGAGAGATATATAAGATCA	120
Db	68346	TCCCTAAACCTGTATAGCCTCCATTCGGAATGATGTGTTCGAGAGATATATAAGATCA	6822
Qy	121	GGAGAGAGAGATTCACAGTTAGCCAAAGTCCAGGCTGTGTCTCTTATTTTATGCA	180
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Qy	241	CATCAACACGAGCTTAAGAAACAGAAATGAGATGCGCATCTGCCCAAGAAAATATGCAG	300
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Qy	301	GAGAGAAATATATATGAAAAATTAACCTTTCCCTTGTTTTAAATTACAGAAAAAATG	360
Db	68106	GAGAGAAATATATATGAAAAATTAACCTTTCCCTTGTTTTAAATTACAGAAAAAATG	6804

Qy	1441	GTTCACCAATTTAGCCGGGCTGGATCTGGACTCGTACCTCAGTATCCACCACCTC	1500
Db	66966	GTTCACCAATTTAGCCGGGCTGGATCTGGACTCGTACCTCAGTATCCACCACCTC	66907
Qy	1501	AGCCTCTTAAAGTGTGGAGATTACAGGATAGTCAACGCGCCGGGCAAGGGTCAAGTGT	1560
Db	66906	AGCCTCTTAAAGTGTGGAGATTACAGGATAGTCAACGCGCCGGGCAAGGGTCAAGTGT	6684
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Db	66846	TTAATPAGGAATAACTTGAATGTTTATTAACCAACAGGGAAACAGACAAAGCTGTGA	66787
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Db	66306	CTTACTTCTGTGAGGTGACATTTCTCATGGAAGCGTGCAGAAAGAAATTTAATAGCA	66247
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Db	66246	GCCAACTTAAACCCAGTGTGGAAGGAAGAAATTAACCACTCTTGAAGATTTGTGGC	66187
Qy	2221	AGCATCCCTTTACAAAGGCCACTCCCTTACGGCCCTGTGCTCATCTGTCGCCCGAGG	2280
Db	66186	AGCATCCCTTTACAAAGGCCACTCCCTTACGGCCCTGTGCTCATCTGTCGCCCGAGG	66127
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Db	66126	CCCCCAAGCCCCGAGTCTTCCAGAGCTCTCTCTCATCATGTCAAGCGCTGCAAGTGGCT	66067
Qy	2341	GCCCTGCTTCCCTGATAGTCTGTGGTGAATGTAGCTGTGAGACCTCTTGGCTCCAGGCT	2400
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Qy	2401	CCAGAAAGGAATGAGAGAGGAACCTAGCTTACCGAGAAATCTGAGAGGGACAGTGTTC	2460
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Qy	2461	CTCAGAGGGAAAGGGGCTCCACGTCACAGAGAAATCCAGAGAGGTGGAGACTGCAAGGAG	2520
Db	65946	CTCAGAGGGAAAGGGGCTCCACGTCACAGAGAAATCCAGAGAGGTGGAGACTGCAAGGAG	65887
Qy	2521	TGGGACGCTGGGGCTGACCGGCTCTAAAGGCGAGAAAGGTGTGAAGGGCCAGGCTGAA	2580



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Qy	241	CATCAACAGAGCTAAGAAACAGSAATGAGTGGGCACTTGCCCAAGSAAATATCCAG	300
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Qy	301	GAGAGCAAAATATATGATGATAAAATAAATCTTTCCCTTTGTTTTTAATTCAGAAAAAATG	360
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Qy	661	AGTATATTAGGCAAGTTGACCATGTTGGCAACCTCCCGCTATATACAGSAAACCTCAAA	720
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Qy	841	GGGACCTGAGGCATTTGCTTTAGSAAAGGCACTTTCTTAGAGATCTTTAGSAAAGCTC	900
Db	841	GGGACCTGAGGCATTTGCTTTAGSAAAGGCACTTTCTTAGAGATCTTTAGSAAAGCTC	900
Qy	901	TTGAAAGATCATGAATTTTAAACCATTTTAAGTATTAACCAATATGCGATGCAATATAG	960
Db	901	TTGAAAGATCATGAATTTTAAACCATTTTAAGTATTAACCAATATGCGATGCAATATAG	960
Qy	961	TTTAGACATGGGTCCTAATTTTATTAAGTCAGAGATCAAGSATAAGTAAAGTGTCCAGCTCC	1020
Db	961	TTTAGACATGGGTCCTAATTTTATTAAGTCAGAGATCAAGSATAAGTAAAGTGTCCAGCTCC	1020
Qy	1021	GGATAGGTCAGAAATCATTTAGAAATCACTGTGTGCCCATCTTAACCTTTTCAGATGATC	1080
Db	1021	GGATAGGTCAGAAATCATTTAGAAATCACTGTGTGCCCATCTTAACCTTTTCAGATGATC	1080
Qy	1081	TGTGATAGGCCCTCACAACAGGCCCATGTGTCTGACCTTAACAACACATCTTACAACTCA	1140
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Qy	1141	GTGCTCACAACATTTTAAAGCTGTCACTAGTAGGTCCTATTAACAAATGCAACTCTCCC	1200
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DB 1441 GTTTCACCATATATAGCCGCGCTGTCTTGAACCTCTGACCTCAGGTTATCCACCACTC 1500  
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DB 1921 TGGGTGTCTGAGCACTGCGCAGCCGCTGCACTGGTGTGTTTATCACTCTCTAG 1980  
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QY 2401 CCGAAGAGAAATGAGAGAGGAACTAGCTTAACCGAATCTGAGAGGAGCAGGTTTC 2460  
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DB 2521 TGGGAGCGTGGGCTGAGCGGCTGCTGAAAGCGAGAGGTAAGGAGGAGGCTGAA 2580  
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QY 2881 TGAAGTCTTTCTTTCTGCTTCTGAGCACTGCTCAGCTGTGAGTGTGAGTGTG 2940  
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QY 2941 GGTGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3000  
DB 2941 GGTGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3000  
QY 3001 ATAAAGCCTTGCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060  
DB 3001 ATAAAGCCTTGCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060  
QY 3061 GATGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120  
DB 3061 GATGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120  
QY 3121 GGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3180  
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PR 11-JAN-1999 US 09/227881.07-MAY-1999 US 09/306828 PI  
THAI D NGUYEN, JON R POLANSKY, PU CHEN, HUA CHEN PC  
C12N15/09, A61K31/573, A61K45/00, A61P27/06, C12N1/15, C12N1/19, PC  
C12N1/21,  
PC C12N5/10, C1201/68, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC  
Nucleic acids, kits, and methods for the diagnosis, prognosis CC  
and

FEATURES

CC treatment of glaucoma and related disorders  
FH Key Location/Qualifiers  
FT source 1..5304  
FT Location/Qualifiers  
1..5304  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 99.1%; Score 5224.4; DB 6; Length 5304;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 5264; Conservative 0; Mismatches 6; Indels 6; Gaps 3;

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DB 61 TCCATAAAGCTGTACCTCCATGGATGTAATGCTTGGCAGAGTGAATGAATCA 120  
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DB 121 GGAAGAAGAGTATCCAGTTCAGCAAGTGTCTCTCTTATTTATGTA 180  
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ORGANISM		Unknown.		
REFERENCE		Unclassified.		
AUTHORS		1 (bases 1 to 5304)		
TITLE		Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H. Nucleic acids,kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders Patent: US 6475724-A 2 05-NOV-2002;		
JOURNAL		Location/Qualifiers		
FEATURES		1..5304		
SOURCE		/mol_type="genomic DNA"		
ORIGIN				
Query Match		99.1%; Score 5224.4; DB 6; Length 5304;		
Best Local Similarity		99.8%; Pred. No. 0;		
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QY		121	GGAAGAAGAGATATCCAGGTTAGCCAACTGTCCAGGCTGTGCTGCTCTTATTTTNGRA	180
Db		121	GGAAGAAGAGATATCCAGGTTAGCCAACTGTCCAGGCTGTGCTGCTCTTATTTTNGRA	180
QY		181	CAGATGTGCTCTGACAGAACCTATTCTTCAGAGAAAATCACATCCAAATATGTAATC	240
Db		181	CAGATGTGCTCTGACAGAACCTATTCTTCAGAGAAAATCACATCCAAATATGTAATC	240
QY		241	CATCAAAACAGAGCTTAAGAAACAGAGATGAGATGGGCACTTGCCCAAGAAAAATCCAG	300
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Db 2641 CTTTTCATCTTTCTCTGCTGAGAGAGAGTCAATTTCTATGAGGAGTGAAGTTC 2700  
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Db 361 ATGAGGACCAAAATCAATGATATAGAAAAACAGCTCAGAAAAAAGATGTTCCTCAATTGG 420  
QY 421 TAATTAAGTATTTTCTCTTGGGAAAGACCTCCATGTGAGCTTGAATGGGAAAATGGGA 480  
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QY 481 AAAGCTAAAAAGCATGATCTGATCAGATCCCAAGTGAATTAATTTAAAAACCAAT 540  
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Db 4321 CTCAAG 4380  
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QY	4861	GGATCCACAGTCCAGATATGTCCTGGCAAGTGAAGTTCTCAATAGTTTCCAAAG	4920
Db	4861	GGATCCACAGTCCCTAGATATGTCCTGGCAAGTGAAGTTCTCAATAGTTTCCAAAG	49200
QY	4921	TGAATGAAATATAACTAGAAATATATCCTTGTGAATCAGACACCAAGTACTCG	4980
Db	4921	TGAATGAAATATAACTAGAAATATATCCTTGTGAATCAGACACCAAGTACTCG	49800
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QY	5041	TAGGAATATATATTTGGGATATGGGTGCAATAATTTGGATATGTTCTTTTAAAGAAATC	5100
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RESULT 2  
US-08-938-669A-3  
Sequence 3, Application US/08938669A  
Patent No. 6171788  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
TITLE OF INVENTION: RELATED DISEASES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue, N.W.  
City: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,669A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/791,154  
FILING DATE: 28-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mendelson, Elliot  
REGISTRATION NUMBER: P-42,878  
REFERENCE/DOCKET NUMBER: 07425-0034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 383-6857

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/ TELEFAX: 202 383-6610
/
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6169 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-938-669A-3

Query Match      100.0%; Score 5271; DB 3; Length 6169;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATCTTTTGACGTTTACCTCAGGCGTATTATGAAGAAATGAGATPACCAATGTGAAG 60
DB      1 ATCTTTGTTCACTTTTCTCCTCAGGCGTATTATGAAGAAATGAGATPACCAATGTGAAG 60

QY      61 TCTTATAA CTGTATAGCCTCCATTCCGATGTATGTTCTTGCGAGAGATATAAGATCA 120
DB      61 TCTTATAA CTGTATAGCCTCCATTCCGATGTATGTTCTTGCGAGAGATATAAGATCA 120

QY      121 GGAAGAGAGAGATCCAGGTAGCCAAATGTCCAGGCTGTGTCTGCTTATTATTAGTA 180
DB      121 GGAAGAGAGAGATCCAGGTAGCCAAATGTCCAGGCTGTGTGTCTGCTTATTATTAGTA 180

QY      181 CAGATGTTCTCCTGACAGAAAGCTATTCTTCAGAAAACATCACATCAATATGTAATC 240
DB      181 CAGATGTTCTCCTGACAGAAAGCTATTCTTCAGAAAACATCACATCAATATGTAATC 240

QY      241 CATCAAAACGAGAGCTTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGAAAATGCCAG 300
DB      241 CATCAAAACGAGAGCTTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGAAAATGCCAG 300

QY      301 GAGAGCAAAATATGATGAAAAATTAACCTTTGCCCTTGTTTAAATTTCAGGAAAAAATG 360
DB      301 GAGAGCAAAATATGATGAAAAATTAACCTTTGCCCTTGTTTAAATTTCAGGAAAAAATG 360

QY      361 ATGAGAGCCAAATATCAATGAATAAGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTG 420
DB      361 ATGAGAGCCAAATATCAATGAATAAGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATTG 420

QY      421 TAATTAGATTGTTGCTTGCGGAAGAGACCTCAATGTGATGCTGATGAGGAAAAATGGAA 480
DB      421 TAATTAGATTGTTGCTTGCGGAAGAGACCTCAATGTGATGCTGATGAGGAAAAATGGAA 480

QY      481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGGATTAATTATTTAAAAACCAT 540
DB      481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGGATTAATTATTTAAAAACCAT 540

QY      541 GGCATCACTCTGGGAGGCAAGTTCAAGAAAGTCAATGTTAGCAAAAGACATPACATPAC 600
DB      541 GGCATCACTCTGGGAGGCAAGTTCAAGAAAGTCAATGTTAGCAAAAGACATPACATPAC 600

QY      601 AGCAAAATCAAAATTCGCAAAATCAGAGAGAAAATGCGGACCTGGGAAAAGCTTCATPAC 660
DB      601 AGCAAAATCAAAATTCGCAAAATCAGAGAGAAAATGCGGACCTGGGAAAAGCTTCATPAC 660

QY      661 AGTATTTAGGAGATTGACCATGTTGCAACACCTCCCGGCTTATACAGGAAACAAAA 720
DB      661 AGTATTTAGGAGATTGACCATGTTGCAACACCTCCCGGCTTATACAGGAAACAAAA 720

QY      721 ATTGACTGAGGCTAGACCGGACTTTCAAGGGAATATGAAAACTGAGAGAAAACAAAA 780
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QY      781 GACATGTTTAAAGCAACAGAACTGTGAGCCTTCAAGACAGCAAGTGCCTTCAGCA 840
DB      781 GACATGTTTAAAGCAACAGAACTGTGAGCCTTCAAGACAGCAAGTGCCTTCAGCA 840

QY      841 GGGAGCCCTGAGGCAATTGCTTTAGGAAGCCAGTTTCTTAPAGGAATCTTAPAGAACTC 900
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Db	4201	GGATTATTAACTTACAGTCCAGAAAGCCTGTGAATTGGAATGAGAAAAATTACATTTT	4260
Qy	4261	TGTTTTTACCACTCTCTACATAAATTTCATTTTATTCATTTGCAATGAGGCATPAA	4320
Db	4261	TGTTTTTACCACTCTCTACATAAATTTCATTTTATTCATTTGCAATGAGGCATPAA	4320
Qy	4321	CTCAAGTGTAAATPACAGTACTGTGATTTTGTTCATTACCAATGGAATCACAGACAT	4380
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Qy	4381	TTATACCTATATTAACAGTGTGCGAGATACGTGTGAATGAAATTTTATATCTGAAACTA	4440
Db	4381	TTATACCTATATTAACAGTGTGCGAGATACGTGTGAATGAAATTTTATATCTGAAACTA	4440
Qy	4441	CTTGAATTATGACCTCTCGTGTGATCTGTGTTTTTAAATATATATAAATCATGTTTAA	4500
Db	4441	CTTGAATTATGACCTCTCGTGTGATCTGTGTTTTTAAATATATATAAATCATGTTTAA	4500
Qy	4501	ATTTTGAATTTTGAATATCATATTTTCATATATCTATTTCTTTGTTATCTATATTTT	4560
Db	4501	ATTTTGAATTTTGAATATCATATTTTCATATATCTATTTCTTTGTTATCTATATTTT	4560
Qy	4561	ATTATATTGAAAACATCTTTCTGAGAAGAGTCCCGAGATTTTCAACATAGGTTCTTG	4620
Db	4561	ATTATATTGAAAACATCTTTCTGAGAAGAGTCCCGAGATTTTCAACATAGGTTCTTG	4620
Qy	4621	CATGACACACACAGAGTAAGACTATTTAGAGCTTAACATTTGACATTTGCTGCTGAGA	4680
Db	4621	CATGACACACACAGAGTAAGACTATTTAGAGCTTAACATTTGACATTTGCTGCTGAGA	4680
Qy	4681	TGCAAGACTGAAATTAAGAAAGTTCTCCCAAGATPACAGATGTTTTTAAAGCTAGAGGGTG	4740
Db	4681	TGCAAGACTGAAATTAAGAAAGTTCTCCCAAGATPACAGATGTTTTTAAAGCTAGAGGGTG	4740
Qy	4741	AGGGGGGAAATCTGCGCGCTTCTATAGGAATGCTTCCCTGGAAGCTGTGAGGCTGCTG	4800
Db	4741	AGGGGGGAAATCTGCGCGCTTCTATAGGAATGCTTCCCTGGAAGCTGTGAGGCTGCTG	4800
Qy	4801	CTTGTGTTTCTGGCGGTGTTATTTTCTCTGTGCTCCGCTACGTTTAAAGACTGTGTT	4860
Db	4801	CTTGTGTTTCTGGCGGTGTTATTTTCTCTGTGCTCCGCTACGTTTAAAGACTGTGTT	4860
Qy	4861	GGATCTCCAGTCTCTACATAGTGCCTGCGACACAGTGAAGTTCTCATGATGTTTGACAG	4920
Db	4861	GGATCTCCAGTCTCTACATAGTGCCTGCGACACAGTGAAGTTCTCATGATGTTTGACAG	4920
Qy	4921	TGAATGGAATATPAACTAGAAATATATCTTGTGAAATCAGACACACAGTATGCTCTG	4980
Db	4921	TGAATGGAATATPAACTAGAAATATATCTTGTGAAATCAGACACACAGTATGCTCTG	4980
Qy	4981	TGTAAAGTGTGAACGT	5040
Db	4981	TGTAAAGTGTGAACGT	5040
Qy	5041	TAGAACTATTTATGGGGATAGGGTGCATAAATTGGAGTGTCTTTTAAAAAGAACTC	5100
Db	5041	TAGAACTATTTATGGGGATAGGGTGCATAAATTGGAGTGTCTTTTAAAAAGAACTC	5100
Qy	5101	CAAAACAACCTTCGGAAGTTATTTTCTAAGATCTTGCCTGAGAGGTAAAGCAACCCC	5160
Db	5101	CAAAACAACCTTCGGAAGTTATTTTCTAAGATCTTGCCTGAGAGGTAAAGCAACCCC	5160
Qy	5161	CTGTGTACAGCCCAACCCAGCTTACAGTGGCACCTGTCTTCCCCCATGAAAGGCTG	5220
Db	5161	CTGTGTACAGCCCAACCCAGCTTACAGTGGCACCTGTCTTCCCCCATGAAAGGCTG	5220
Qy	5221	GCTGCCAGATATATPAACTCTCTGTGAAGCTTGGGACATGAGCAGCAAGG	5271
Db	5221	GCTGCCAGATATATPAACTCTCTGTGAAGCTTGGGACATGAGCAGCAAGG	5271

RESULT 3  
US-09-306-828-3  
Sequence 3, Application US/09306828  
Patent No. 6475724  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
APPLICANT: Chen, Pu  
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And  
CURRENT APPLICATION NUMBER: US/09/306,828  
CURRENT FILING DATE: 1999-05-07  
EARLIER APPLICATION NUMBER: US 09/227,881  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO: 3  
LENGTH: 6169  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-828-3

Query Match 100.0%; Score 5271; DB 4; Length 6169;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCTTGTCAGTTTACCTCAGGCGCTATTGAAATGATGATACCAATGTGAAG 60  
DB 1 ATCTTGTCAGTTTACCTCAGGCGCTATTGAAATGATGATACCAATGTGAAG 60  
QY 61 TCCTATAAAGCTGATAGCTTCATTCGATGATGTTCTTGAGAGATGATAAGATCA 120  
DB 61 TCCTATAAAGCTGATAGCTTCATTCGATGATGTTCTTGAGAGATGATAAGATCA 120  
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DB 121 GGAAGAGAGATACCAAGCTTACGAGAGTGCAGGCTGCTGCTTATTTTGA 180  
QY 181 CAGATGTCCTCTGACAGAGCTATTCTCAGGAAACATCACATATGATGTAATC 240  
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QY 241 CATCAACAGAGAGCTAGAGAAACAGAGATGAGATGAGGAGCTTGGCCCAAGGAAATGCCAG 300  
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QY 241 CATCAACAGAGAGCTAGAGAAACAGAGATGAGATGAGGAGCTTGGCCCAAGGAAATGCCAG 300  
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QY 301 GAGAGCAATATGATGAGAAATGAACTTTTCCCTGTTTATTTTCAAGAAATG 360  
DB 301 GAGAGCAATATGATGAGAAATGAACTTTTCCCTGTTTATTTTCAAGAAATG 360  
QY 361 ATGAGAGCAATATGATGAGAAATGAACTTTTCCCTGTTTATTTTCAAGAAATG 420  
DB 361 ATGAGAGCAATATGATGAGAAATGAACTTTTCCCTGTTTATTTTCAAGAAATG 420  
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DB 1621 TTAATTAAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATG 1680  
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QY 1741 CACCATGCTTTTGTGTAAGCTTCAATGATGATGATGATGATGATGATGATGATG 1800

Db 1741 CACCATGCTTTGNGGTAAGCCTCCACATGCTTACTGAATAAGATATACATAAAGTAG 1800  
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGAGAGGGGCATTAACCCAGAGACTCT 1860  
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGAGAGGGGCATTAACCCAGAGACTCT 1860  
Qy 1861 TGAAGCCCCGGAGAGAGTTTCTCTCCAGCTGGGGAGCCCTGCAAGACCCGGGGTCC 1920  
Db 1861 TGAAGCCCCGGAGAGAGTTTCTCTCCAGCTGGGGAGCCCTGCAAGACCCGGGGTCC 1920  
Qy 1921 TGGGTGTCTGAGCAACCTGCGACGCCGTGCACTGTGTGTGTGTATCACTCTTAGS 1980  
Db 1921 TGGGTGTCTGAGCAACCTGCGACGCCGTGCACTGTGTGTGTGTATCACTCTTAGS 1980  
Qy 1981 GACCTGTGCTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
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Db 2101 CTAACCTGTGTAGAGTGAAGTTCTCATGTGAAACGTGCAAGAAATTAATAGCA 2160  
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Db 2161 GCCAAGCTTAAACCCAGTGTGAAAGAAAGAAATTAACCATCTTGAAGATTTGCGC 2220  
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Db 2281 CCCCAGAGCCGAGTCTTCAAGACCTCTCTCTCATCACTGCAAGCGTGTGAGCTGGCT 2340  
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QY	3361	AGAAATGAATCTTTAGAGCAAATGCTGTTCTCCACATCTGGAGGGAGATCTGCCAGGCG	4020
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QY	4021	AGTTGGAATATTTACTTCACAGATTAAGCACTGTGTGTGGTAATTAACAATPAAGT	4080
Db	4021	AGTTGGAATATTTACTTCACAGATTAAGCACTGTGTGTGGTAATTAACAATPAAGT	4080
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Db	4081	TGCTCAAGGCAATCATTTATCAAGGCTTAAAGTACTTCTGACAGTTTGGATAT	4140
QY	4141	TTATGGCTATTTGSCATTTGCTTTTGTGTTTCTCTTGGTTATTTATGTAAAGAG	4200
Db	4141	TTATGGCTATTTGSCATTTGCTTTTGTGTTTCTCTTGGTTATTTATGTAAAGAG	4200
QY	4201	GGATTATTTAACTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTAACATTT	4260
Db	4201	GGATTATTTAACTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAATTAACATTT	4260
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QY	4321	CTCAAGGTGATTAACAGTACCTGTGATTTTGTCAATTAACAATAGAAATCACAGCATT	4380
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Db	4381	TTATATCTATTAACAGTGTGTGCGAATACGCTGTGAATGAAATATTTATCTCAAAAGTA	4440
QY	4441	CTTGAATATTAAGCCTCCTGCTGATCTTGTGTTTAAACATATTAATAAAACATGTTAAA	4500
Db	4441	CTTGAATATTAAGCCTCCTGCTGATCTTGTGTTTAAACATATTAATAAAACATGTTAAA	4500
QY	4501	ATTTTGATATTTTGATTAATCATATTTCTATACATTTGTTCCCTTGTATCTATATTTT	4560
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Db	4681	TGCAAGACTGAATTAAGAAAGTCTCCCAAGATTAACAGATTTGTTTAAAGCTAGGGGTG	4740
QY	4741	AAGGGGGGAATCTGCGGCTTCTATTAAGAAATGCTCTCCTGAGAGCCTGGTAGGGGCTGTC	4800
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QY	4801	CTTGTGTTCTGCTGCTGCTATATTTTCTCTGTCCTCCGTCAAGCTTAAAGAACTGTGTT	4860
Db	4801	CTTGTGTTCTGCTGCTGCTATATTTTCTCTGTCCTCCGTCAAGCTTAAAGAACTGTGTT	4860
QY	4861	GGATCTCCAGTTCCTAGCATATGCTGTGCAAGTGGAGGTTCTCAATGAATTTGACAG	4920
Db	4861	GGATCTCCAGTTCCTAGCATATGCTGTGCAAGTGGAGGTTCTCAATGAATTTGACAG	4920
QY	4921	TGAATGAAATATTAACCTAGAAATATATCTCTGTTGAAATAGGCAACACATAGCTCGG	4980
Db	4921	TGAATGAAATATTAACCTAGAAATATATCTCTGTTGAAATAGGCAACACATAGCTCGG	4980
QY	4981	TGTAATGTGTGTAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAACCAAGTGTAGATA	5040
Db	4981	TGTAATGTGTGTAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAACCAAGTGTAGATA	5040
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DB	Sequence	Score	DB	Length
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QY	5101 CAACAGACTCTGGAAGCTTATTTCTAAGATCTTGTGGCAGCGTGAAGGCAACCC	99.9%	5100	5100
DB	5101 CAACAGACTCTGGAAGCTTATTTCTAAGATCTTGTGGCAGCGTGAAGGCAACCC	99.9%	5100	5100
QY	5161 CTTGTGCAACCCCAACCGCTGACGAGGCTGATGTTCTTTCCCAAGAGGCTG	99.9%	5160	5160
DB	5161 CTTGTGCAACCCCAACCGCTGACGAGGCTGATGTTCTTTCCCAAGAGGCTG	99.9%	5160	5160
QY	5221 GCTCCCAATATATATAAAGCTCTGTGAGCTGGGATGAGCCAGCAAG	99.9%	5220	5220
DB	5221 GCTCCCAATATATATAAAGCTCTGTGAGCTGGGATGAGCCAGCAAG	99.9%	5220	5220

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Db 121 GGAAGAGAGATCCAGCTTAGCAAGTGTCCAGGCTGTGTCTTATTTAGTGA 180  
QY 181 CAGATGTGCTCCGACAGAGGCTATTTCTCAGAGAAACATCCATCCATATGTAATC 240  
Db 181 CAGATGTGCTCCGACAGAGGCTATTTCTCAGAGAAACATCCATCCATATGTAATC 240  
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## RESULT 5

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US-09-306-828-1
Sequence 1, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Pu
APPLICANT: Chen, Hua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
CURRENT APPLICATION NUMBER: US/09/306,828
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/227,881
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 1
LENGTH: 5300
TYPE: DNA

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/ ORGANISM: Homo sapiens
US-09-306-828-1
Query Match 99.5%; Score 5246.4; DB 4; Length 5300;
Base Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
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3781 TAAAGCCAAACAGATTCAAGCTTAGCTTGTGCTGCTATATGATGGTTTTTGAATAAT 3840  
3781 TAAAGCCAAACAGATTCAAGCTTAGCTTGTGCTGCTATATGATGGTTTTTGAATAAT 3840  
3841 CATTCAGGATGTTTATCTATCTGATTCAGAAAAATGAGACTAGAACCTTTGGTCACTG 3900  
3841 CATTCAGGATGTTTATCTATCTGATTCAGAAAAATGAGACTAGAACCTTTGGTCACTG 3900  
3901 TAAACAAACACCCAGTGTAAATGTTCAAGTTCAAGCTTAAGTCAAGAACCAATCAAA- 3959  
3901 TAAACAAACACCCAGTGTAAATGTTCAAGTTCAAGCTTAAGTCAAGAACCAATCAAA- 3959  
3901 TAAACAAACACCCAGTGTAAATGTTCAAGTTCAAGCTTAAGTCAAGAACCAATCAAA- 3959  
3960 AAGATAGAACTTTAGAGCAAACTGTTCTCAACTCTGAGAGTGAATCTGCCAGG 4019  
3960 AAGATAGAACTTTAGAGCAAACTGTTCTCAACTCTGAGAGTGAATCTGCCAGG 4019  
3961 AAGATAGAACTTTAGAGCAAACTGTTCTCAACTCTGAGAGTGAATCTGCCAGG 4019  
3961 AAGATAGAACTTTAGAGCAAACTGTTCTCAACTCTGAGAGTGAATCTGCCAGG 4019  
4020 CAGTTGGAAATATTTACTTCAAGATGACCTGTTGGTATTAACAATTAAG 4079  
4020 CAGTTGGAAATATTTACTTCAAGATGACCTGTTGGTATTAACAATTAAG 4079  
4080 TTGCTCAAGAGAACTATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTGGTAAT 4139  
4080 TTGCTCAAGAGAACTATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTGGTAAT 4139  
4140 TTATTTGGCTATTTGGCATTTGTTTGTCTTTCTCTTTGGGTTATTAATGTAAGA 4199  
4140 TTATTTGGCTATTTGGCATTTGTTTGTCTTTCTCTTTGGGTTATTAATGTAAGA 4199  
4140 TTATTTGGCTATTTGGCATTTGTTTGTCTTTCTCTTTGGGTTATTAATGTAAGA 4199  
4200 GGGATTTATTAACCTTACAGTCCAGAAAGCTGTGAATTTGAATGAGAGAAAAATTAATTT 4259  
4200 GGGATTTATTAACCTTACAGTCCAGAAAGCTGTGAATTTGAATGAGAGAAAAATTAATTT 4259  
4260 TTGTTTACACCTTCTAATTAATTTAATTTATTTGCAATTTGGAGATAGGCATTA 4319

4260 TTGTTTACACCTTCTAATTAATTTAATTTATTTGCAATTTGGAGATAGGCATTA 4319  
4320 ACTCAAGTGGTAATTAACAGTACCTGATTTTGTTCATTACCAATAGAAATCAGAGCAT 4379  
4320 ACTCAAGTGGTAATTAACAGTACCTGATTTTGTTCATTACCAATAGAAATCAGAGCAT 4379  
4380 TTATTTCTATTTAAGTGTGAGATAGAGTGAATGAATAATTTATCTAAACT 4439  
4380 TTATTTCTATTTAAGTGTGAGATAGAGTGAATGAATAATTTATCTAAACT 4439  
4440 ACTTGAATTTAGACCTCTGCTGATCTGTTTAAATTAATTAATTAATTAATTAATTAAT 4499  
4440 ACTTGAATTTAGACCTCTGCTGATCTGTTTAAATTAATTAATTAATTAATTAATTAAT 4499  
4500 AATTTGAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 4559  
4500 AATTTGAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 4559  
4560 TATATATTTGAAACATCTTTCTGAGAGAGTCCCAAGATTTTCAACCAAGAGGTTCTG 4619  
4560 TATATATTTGAAACATCTTTCTGAGAGAGTCCCAAGATTTTCAACCAAGAGGTTCTG 4619  
4620 GCATGACACACACAGAGTAAAGCTGATTTAGAGCTTAACATTGACATTGTCCTGAG 4679  
4620 GCATGACACACACAGAGTAAAGCTGATTTAGAGCTTAACATTGACATTGTCCTGAG 4679  
4680 ATGCAAGACTGAATTTAAGAGTCTCCCAAGATTAACAGTGTTTTAAAGCTAGGAGT 4739  
4680 ATGCAAGACTGAATTTAAGAGTCTCCCAAGATTAACAGTGTGTTTTAAAGCTAGGAGT 4739  
4740 GAGGGGGGAAATCTGCGCTTTCTATAGAAATGCTCTCTGAGAGCTGTAGGCTCTGT 4799  
4740 GAGGGGGGAAATCTGCGCTTTCTATAGAAATGCTCTCTGAGAGCTGTAGGCTCTGT 4799  
4800 CCTGTGTTCTGAGGCTGTATTTTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 4859  
4800 CCTGTGTTCTGAGGCTGTATTTTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 4859  
4800 CTTTGTGTTCTGAGGCTGTATTTTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 4859  
4860 TEGATCTCAGTCTCTGACATAGTCTGAGAGTCTGAGAGTCTCAATGAGTTTGCAGA 4919  
4860 TEGATCTCAGTCTCTGACATAGTCTGAGAGTCTGAGAGTCTCAATGAGTTTGCAGA 4919  
4860 TEGATCTCAGTCTCTGACATAGTCTGAGAGTCTGAGAGTCTCAATGAGTTTGCAGA 4919  
4920 GTGATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4979  
4920 GTGATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4979  
4980 GTGATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4979  
4980 GTGATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4979  
5040 ATAGAACTATTAATTTGGGATAGGAGTGAATTAATTTGGGATAGGAGTCTTTTAAAAAGAACT 5099  
5040 ATAGAACTATTAATTTGGGATAGGAGTGAATTAATTTGGGATAGGAGTCTTTTAAAAAGAACT 5099  
5100 CCAACAGACTCTGGAAGGTTATTTTCTAAGAACTCTGCTGAGAGGCTGAGAGGCAACC 5159  
5100 CCAACAGACTCTGGAAGGTTATTTTCTAAGAACTCTGCTGAGAGGCTGAGAGGCAACC 5159  
5100 CCAACAGACTCTGGAAGGTTATTTTCTAAGAACTCTGCTGAGAGGCTGAGAGGCAACC 5159  
5160 CCTGTGACAGAGCCCAAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCT 5219  
5160 CCTGTGACAGAGCCCAAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCTCAGAGGCT 5219  
5220 GGGTCCCAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5271  
5220 GGGTCCCAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5271

RESULT 6  
US-08-699A-2  
; Sequence 2, Application US/08938669A  
; Parent No. 6171788  
; GENERAL INFORMATION:

QY	422	TAAATGAATTTGTCCTTGGGAAGACCTCCAGTGTAGCTGTATGGAAAAATGGGA	480
QY	421	TAAATGAATTTGTCCTTGGGAAGACCTCCAGTGTAGCTGTATGGAAAAATGGGA	480
QY	481	AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGATATATATTTAAAAACCAT	540
Db	481	AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGATATATATTTAAAAACCAT	540
QY	541	GGATCACTCTGGGGAGGGAAGTTCAGGAAGGTCATGTAGCAAAAGCATATAA	600
Db	541	GGATCACTCTGGGGAGGGAAGTTCAGGAAGGTCATGTAGCAAAAGCATATAA	600
QY	601	AGCAAAATCAAAATTCGCAAAATGCAGAGAAAATGGGACTGGAAAACCTTCA	660
Db	601	AGCAAAATCAAAATTCGCAAAATGCAGAGAAAATGGGACTGGAAAACCTTCA	660
QY	661	AGTATTTAGGCACTTGACATGTTGGCAACCTCCCCCGCTATACAGGGAACAAAA	720
Db	661	AGTATTTAGGCACTTGACATGTTGGCAACCTCCCCCGCTATACAGGGAACAAAA	720
QY	721	ATTGACTGGGCTAAGCCTGACTTTCAAGGGAATATGAAAACTGAGACAAAA	780
Db	721	ATTGACTGGGCTAAGCCTGACTTTCAAGGGAATATGAAAACTGAGACAAAA	780
QY	781	GACATGTTAAAGCAACCAACATTTGAGCTTCAAGAGACAGATGCCCTCAGCA	840
Db	781	GACATGTTAAAGCAACCAACATTTGAGCTTCAAGAGAGAGAGAGAGTGCCTCAGCA	840
QY	841	GGAGCCCTGAGGCAATTTGGCTTTAGGAAGGCACTTTCTTAAGAACTTAA	900
Db	841	GGAGCCCTGAGGCAATTTGGCTTTAGGAAGGCACTTTCTTAAGAACTTAA	900
QY	901	TTGAAAGATCATGAAATTTTAAACATTTTAAAGTAAACAAATATGCGATCAT	960
Db	901	TTGAAAGATCATGAAATTTTAAACATTTTAAAGTAAACAAATATGCGATCAT	960
QY	961	TTTGAATGATGGTCCCAATTTTAAAGTGAAGATCAAGATATAGTCCAGTCC	1020
Db	961	TTTGAATGATGGTCCCAATTTTAAAGTGAAGATCAAGATATAGTCCAGTCC	1020
QY	1021	GGATAGGTCAGAAATCATTTAGAAATCACTGTGCCCATCTAACTTTTCA	1080
Db	1021	GGATAGGTCAGAAATCATTTAGAAATCACTGTGCCCATCTAACTTTTCA	1080
QY	1081	TGTCATAGCCTCTCAACAAGGCCCATGTGTCTGACCTTACACCAATCTAAC	1140
Db	1081	TGTCATAGCCTCTCAACAAGGCCCATGTGTCTGACCTTACACCAATCTAAC	1140
QY	1141	GTGCTCAACCATTTGTTAAGTGTACGTCTAGTATGATGATGATGATGATGAT	1200
Db	1141	GTGCTCAACCATTTGTTAAGTGTACGTCTAGTATGATGATGATGATGATGAT	1200
QY	1201	TGTGAGGCCATCCCGCTCCACAGAAATCTCCCATCTTGAATTTCTGATCAG	1260
Db	1201	TGTGAGGCCATCCCGCTCCACAGAAATCTCCCATCTTGAATTTCTGATCAG	1260
QY	1261	TACAGCCAGAAAGTCCGTAAGGGGTGAGAGTGTGTCTTACACTTACTGAT	1320
Db	1261	TACAGCCAGAAAGTCCGTAAGGGGTGAGAGTGTGTCTTACACTTACTGAT	1320
QY	1321	ACCTGAGTCACTGCAACCTCTGCTCCAGGTTCAAGCAATTCCTGTCTAG	1380
Db	1321	ACCTGAGTCACTGCAACCTCTGCTCCAGGTTCAAGCAATTCCTGTCTAG	1380
QY	1381	CGCTAGTGGGATCTACAGGGGCAAGCCGGCTATTTGTATTTAGTAGAGAT	1440
Db	1381	CGCTAGTGGGATCTACAGGGGCAAGCCGGCTATTTGTATTTAGTAGAGAT	1440
QY	1441	GTTCACCATTTAGCCCGCTGTCTTGAATCTCTGACCTCAGATGATCACC	1500
Db	1441	GTTCACCATTTAGCCCGCTGTCTTGAATCTCTGACCTCAGATGATCACC	1500
QY	1501	AGCTCTAAAGTGTGGGATTTAAGCATATAGTACCGGCCCGGCAAGGTCAG	1560

Db 1501 AGCTCTCTAAAGTGTCTGGGATTACAGGCAAGATCAACCGGCCCGCCAGGGGTCAAGTCT 1560  
Qy 1561 TTAATTAAGGAATTAAGTGAATGGTTTACTTAACCAACAGGAAACAGACAAAAGCTGTGA 1620  
Db 1561 TTAATTAAGGAATTAAGTGAATGGTTTACTTAACCAACAGGAAACAGACAAAAGCTGTGA 1620  
Qy 1621 TTAATTAAGGAATTAAGTGAATGGTGAATGGTSCATAGACTGCCCTAGTCCAGAC 1680  
Db 1621 TTAATTAAGGAATTAAGTGAATGGTGAATGGTSCATAGACTGCCCTAGTCCAGAC 1680  
Qy 1681 CACTGTCTCTCATCACTTTTCTCCCTCATCTTCATTTTCAAGCTTAAGTTTAACTTTTAT 1740  
Db 1681 CACTGTCTCTCATCACTTTTCTCCCTCATCTTCATTTTCAAGCTTAAGTTTAACTTTTAT 1740  
Qy 1741 CACCATCTTTTGTGTGAAGCTCTCAACATGTACTGAATTAAGATPATCAATAACTAG 1800  
Db 1741 CACCATCTTTTGTGTGAAGCTCTCAACATGTACTGAATTAAGATPATCAATAACTAG 1800  
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGAGAGAGGCAATACCCAGAGACTCT 1860  
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGAGAGAGGCAATACCCAGAGACTCT 1860  
Qy 1861 TGAAGCCCGCGGAGAGGTTTCTCTCAAGCTGGGGAGCCCTGCAACACCCGGGGTCC 1920  
Db 1861 TGAAGCCCGCGGAGAGGTTTCTCTCAAGCTGGGGAGCCCTGCAACACCCGGGGTCC 1920  
Qy 1921 TGGGTGTCTGAGCAACTGTGCAGCCCGTGCACATGTGTTTGTATCACTCTAG 1980  
Db 1921 TGGGTGTCTGAGCAACTGTGCAGCCCGTGCACATGTGTTTGTATCACTCTAG 1980  
Qy 1981 GACCTGTGTCTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
Db 1981 GACCTGTGTCTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
Qy 2041 TATTGAGTCTTATCTGCTCAGACACAGAGACAAAATGTGAGCAAGAGACTGAC 2100  
Db 2041 TATTGAGTCTTATATCTGCTCAGACACAGAGACAAAATGTGAGCAAGAGACTGAC 2100  
Qy 2101 CCTACTGTGTGAGGTGACAGTTTCTCATGAGAAAGCTGCAAGAAATTAATAGCCA 2160  
Db 2101 CCTACTGTGTGAGGTGACAGTTTCTCATGAGAAAGCTGCAAGAAATTAATAGCCA 2160  
Qy 2161 GCCAATCTTAACCCAGTGTGTAAGAAAGAAATTAACCATCTGTAAGAAATGTGCGC 2220  
Db 2161 GCCAATCTTAACCCAGTGTGTAAGAAAGAAATTAACCATCTGTAAGAAATGTGCGC 2220  
Qy 2221 AGCATCTCTTAACAAGGCCACTCCCTAGCGCCCTGCTGCTGCATCGTGCAGAGG 2280  
Db 2221 AGCATCTCTTAACAAGGCCACTCCCTAGCGCCCTGCTGCTGCATCGTGCAGAGG 2280  
Qy 2281 CCCCCAAGCCGAGTCTTCCAGAGCTCTCTCTCCATCATGTCACAGCGCTGAGTGGCCT 2340  
Db 2281 CCCCCAAGCCGAGTCTTCCAGAGCTCTCTCTCCATCATGTCACAGCGCTGAGTGGCCT 2340  
Qy 2341 GCTGTGCTTCCGCTGATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400  
Db 2341 GCTGTGCTTCCGCTGATGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400  
Qy 2401 CCAGAAAGAAATGAGAGGAAATTAAGTCTTAACGAGAAATCTGAGAGGAAAGCTGTTTC 2460  
Db 2401 CCAGAAAGAAATGAGAGGAAATTAAGTCTTAACGAGAAATCTGAGAGGAAAGCTGTTTC 2460  
Qy 2461 CTCAAGAGGAAAGGAGGCTCTCAAGTCTCAAGAGAAATTCAGAGAGTGGGAACTGAGAGAG 2520  
Db 2461 CTCAAGAGGAAAGGAGGCTCTCAAGTCTCAAGAGAAATTCAGAGAGTGGGAACTGAGAGAG 2520  
Qy 2521 TGGGAGCGTGGGCTGAGCGGCTGTGAAGGAGAGAGGTTGAAAAGGCAAGGCTGAA 2580  
Db 2521 TGGGAGCGTGGGCTGAGCGGCTGTGAAGGAGAGAGGTTGAAAAGGCAAGGCTGAA 2580  
Qy 2581 GGTGCGCAGATTTAGT 2640  
Db 2581 GGTGCGCAGATTTAGT 2640

Db 2581 GGTGCGCAGATTTAGT 2640  
Qy 2641 CTTTATATCTTTCTCTGCTTGGAGAGAGAGTCTTATTTCAATGAAGGATGCAAGTTTC 2700  
Db 2641 CTTTATATCTTTCTCTGCTTGGAGAGAGAGTCTTATTTCAATGAAGGATGCAAGTTTC 2700  
Qy 2701 ATTAAGTCAAGCTGTAAATTCAGAGGAGTGTGATGGGTTTCTCTCAAGAGGCTTAT 2760  
Db 2701 ATTAAGTCAAGCTGTAAATTCAGAGGAGTGTGATGGGTTTCTCTCAAGAGGCTTAT 2760  
Qy 2761 TTAATGGAATTAAGAAACGAGCTCATTTCTTAGGCCGTTAATTCACGAAAGGTGAC 2820  
Db 2761 TTAATGGAATTAAGAAACGAGCTCATTTCTTAGGCCGTTAATTCACGAAAGGTGAC 2820  
Qy 2821 TGGAGCTTTTCTTCAAGTCTCTGAGCAACTACTAGCCCTGATGAGCTTGGCTTA 2880  
Db 2821 TGGAGCTTTTCTTCAAGTCTCTGAGCAACTACTAGCCCTGATGAGCTTGGCTTA 2880  
Qy 2881 TGCAGACGCTGAAAAACCTTGAATCAGAGACTCGATTTTCTTCTGTGTGTGCAATT 2940  
Db 2881 TGCAGACGCTGAAAAACCTTGAATCAGAGACTCGATTTTCTTCTGTGTGTGCAATT 2940  
Qy 2941 GGTGTGTGTGTGACCGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGCT 3000  
Db 2941 GGTGTGTGTGTGACCGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGCT 3000  
Qy 3001 ATTAAGACCTTTGAGCTCTGT 3060  
Db 3001 ATTAAGACCTTTGAGCTCTGT 3060  
Qy 3061 GGATGTGAGAGGAG 3120  
Db 3061 GGATGTGAGAGGAG 3120  
Qy 3121 GAGCAG 3180  
Db 3121 GAGCAG 3180  
Qy 3181 CAGAGCCGAGAGCCCAATGCTTCAAGAAAGCTCAATGAACCCAGACAGCCATTTTCT 3240  
Db 3181 CAGAGCCGAGAGCCCAATGCTTCAAGAAAGCTCAATGAACCCAGACAGCCATTTTCT 3240  
Qy 3241 TCCCTAAGCATTAAGCAATGGCATTTGCAATTAACAAAAGATGAGAGAGAGAGAGAGAG 3300  
Db 3241 TCCCTAAGCATTAAGCAATGGCATTTGCAATTAACAAAAGATGAGAGAGAGAGAGAGAG 3300  
Qy 3301 GGATGCTTTTCTGAGATTCAAAACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360  
Db 3301 GGATGCTTTTCTGAGATTCAAAACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360  
Qy 3361 TTAATCTTTTCAAGCTGACAGCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420  
Db 3361 TTAATCTTTTCAAGCTGACAGCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420  
Qy 3421 AGTACCTGACAG 3480  
Db 3421 AGTACCTGACAG 3480  
Qy 3481 AAGATCTGACAG 3540  
Db 3481 AAGATCTGACAG 3540  
Qy 3541 GTTCTAG 3600  
Db 3541 GTTCTAG 3600  
Qy 3601 CCTGATTTCTAATCTAATTTTCTTTTCAAGCTGAGTAATTTGAGCAAGTCAAG 3660  
Db 3601 CCTGATTTCTAATCTAATTTTCTTTTCAAGCTGAGTAATTTGAGCAAGTCAAG 3660  
Qy 3661 GTAGTAATCTAG 3720  
Db 3661 GTAGTAATCTAG 3720





Db 181 CAGATGTGCTCCTGACAGAAAGCTATTCTTCAGAAACATCACATCAATATGTGTAATC 240  
QY 241 CATCAAAACGAGAGCTAGAAAACAGAAATGAGATGGGCACTTGGCCCAAGAAAAATGCGAG 300  
Db 241 CATCAAAACGAGAGCTAGAAAACAGAAATGAGATGGGCACTTGGCCCAAGAAAAATGCGAG 300  
QY 301 GAGAGCAAAATATGATGAAAAATAACTTTCCCTTTGTTTAAATTTTCAGAAAAATG 360  
Db 301 GAGAGCAAAATATGATGAAAAATAACTTTCCCTTTGTTTAAATTTTCAGAAAAATG 360  
QY 361 ATGAGAGCAAAATATGATGAAAAATGAGAAAAACAGCTCAAGAAAAATGTTCCAAATGG 420  
Db 361 ATGAGAGCAAAATATGATGAAAAATGAGAAAAACAGCTCAAGAAAAATGTTCCAAATGG 420  
QY 421 TAAATTAAGTATTTGTTCTTGGGAAAGAGACCTTCATGTAGAGCTTGATGGAAAAATGG 480  
Db 421 TAAATTAAGTATTTGTTCTTGGGAAAGAGACCTTCATGTAGAGCTTGATGGAAAAATGG 480  
QY 481 AAACGTCAAAAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
Db 481 AAACGTCAAAAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
QY 541 GGCATCACTCTGGGAGGAGCAAGTTCAGAAAGCTCATGTAGCAAGACATACATAC 600  
Db 541 GGCATCACTCTGGGAGGAGCAAGTTCAGAAAGCTCATGTAGCAAGACATACATAC 600  
QY 601 AGCAAAATCAAAATTCGCAAAATGCAAGGAAAAATGGGAACTGGGAAAGCTTCATAC 660  
Db 601 AGCAAAATCAAAATTCGCAAAATGCAAGGAAAAATGGGAACTGGGAAAGCTTCATAC 660  
QY 661 AGTATTAAGGAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Db 661 AGTATTAAGGAGTTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
QY 721 ATTGATGAGGCTTAAGCTTGAAGCTTTCAGAAAGCTGATGATGATGATGATGATGAT 780  
Db 721 ATTGATGAGGCTTAAGCTTGAAGCTTTCAGAAAGCTGATGATGATGATGATGATGAT 780  
QY 781 GATATGTTTAAAGGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
Db 781 GATATGTTTAAAGGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
QY 841 GGGACCTGAGGATTTGCTTTAGAGAGGCGCATTTTCTTAAGAAATCTTAAGAAATC 900  
Db 841 GGGACCTGAGGATTTGCTTTAGAGAGGCGCATTTTCTTAAGAAATCTTAAGAAATC 900  
QY 901 TTTAAAGATCAATGATTTTAAACATTTTAAATTAAGTAAAGTAAAGTAAAGTAAAGT 960  
Db 901 TTTAAAGATCAATGATTTTAAACATTTTAAATTAAGTAAAGTAAAGTAAAGTAAAGT 960  
QY 961 TTTAGACATGAGGCTCAATTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1020  
Db 961 TTTAGACATGAGGCTCAATTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1020  
QY 1021 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
Db 1021 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
QY 1081 TGTATAGGCTTCACACAGAGGCGGATGATGATGATGATGATGATGATGATGATGAT 1140  
Db 1081 TGTATAGGCTTCACACAGAGGCGGATGATGATGATGATGATGATGATGATGATGAT 1140  
QY 1141 GTGCTCAACCAATGTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1200  
Db 1141 GTGCTCAACCAATGTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1200  
QY 1201 TGTGAGGCTTCACACAGAGGCGGATGATGATGATGATGATGATGATGATGATGAT 1260  
Db 1201 TGTGAGGCTTCACACAGAGGCGGATGATGATGATGATGATGATGATGATGATGAT 1260  
QY 1261 TACAGCAAAAGCTCCGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 1320  
Db 1261 TACAGCAAAAGCTCCGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 1320

QY 1321 ACCTAGCTCACTGCAACCTCTGCTCCAGAGTTCAAGCAATTTCTCTGTCTCAGCTCC 1380  
Db 1321 ACCTAGCTCACTGCAACCTCTGCTCCAGAGTTCAAGCAATTTCTCTGTCTCAGCTCC 1380  
QY 1381 CCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTGTATGTTTGTATGATGATG 1440  
Db 1381 CCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTGTATGTTTGTATGATGATGATG 1440  
QY 1441 GTTTACCATATTTAGCCCGGCTGGCTGAACTCTGACCTCAGGATGATCACCACCTC 1500  
Db 1441 GTTTACCATATTTAGCCCGGCTGGCTGAACTCTGACCTCAGGATGATCACCACCTC 1500  
QY 1501 AGCTCTTAAAGTGTGGGATTTAAGCAGATGATCACCAGCCCGGCTCAAGGCTCAGTGT 1560  
Db 1501 AGCTCTTAAAGTGTGGGATTTAAGCAGATGATCACCAGCCCGGCTCAAGGCTCAGTGT 1560  
QY 1561 TTAATTAAGGATTAATCTTAATGTTTAAAGCAAGGAAAAACAGCAAAAGCTGTGA 1620  
Db 1561 TTAATTAAGGATTAATCTTAATGTTTAAAGCAAGGAAAAACAGCAAAAGCTGTGA 1620  
QY 1621 TAAATTAAGGATTTCTTGGGATGAGGAAATGATGATGATGATGATGATGATGATGAT 1680  
Db 1621 TAAATTAAGGATTTCTTGGGATGAGGAAATGATGATGATGATGATGATGATGATGAT 1680  
QY 1681 CACTGCTCTCATCACTTTCTTCCCTCATCTCATCTTTCAGGCTAAGTATGATTTAT 1740  
Db 1681 CACTGCTCTCATCACTTTCTTCCCTCATCTCATCTTTCAGGCTAAGTATGATTTAT 1740  
QY 1741 CACATGCTTTTGTGTAAGCTCCATCATGTTACTGAATTAAGATATCATTAATCTAG 1800  
Db 1741 CACATGCTTTTGTGTAAGCTCCATCATGTTACTGAATTAAGATATCATTAATCTAG 1800  
QY 1801 TTCCATTTGGGCGCATCTGTGTGTGTATAGGAGAGGAGGATACCCAGAGACTCTCT 1860  
Db 1801 TTCCATTTGGGCGCATCTGTGTGTGTATAGGAGAGGAGGATACCCAGAGACTCTCT 1860  
QY 1861 TGAACCCCGGAGAGGTTTCTCTCAGCTGGGAGGCTCTGAAAGCAACCGGAGCTC 1920  
Db 1861 TGAACCCCGGAGAGGTTTCTCTCAGCTGGGAGGCTCTGAAAGCAACCGGAGCTC 1920  
QY 1921 TGGGTGCTTAGCAACTGCGACCGGCTCACTGCTGTTGTTGTTATCATCTCTAG 1980  
Db 1921 TGGGTGCTTAGCAACTGCGACCGGCTCACTGCTGTTGTTGTTATCATCTCTAG 1980  
QY 1981 GACCTGCTCTTCAATTTCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 2040  
Db 1981 GACCTGCTCTTCAATTTCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 2040  
QY 2041 TATTGAGTACTTATCTGCGCAGACACCAAGACAAATGATGAGCAAAAGCACTGAC 2100  
Db 2041 TATTGAGTACTTATCTGCGCAGACACCAAGACAAATGATGAGCAAAAGCACTGAC 2100  
QY 2101 CCTACCTTCGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160  
Db 2101 CCTACCTTCGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160  
QY 2161 GCGAACTTAAACCAAGTCTGAAAGAAAGAAATTAACCATCTTGAAGATTTGCGC 2220  
Db 2161 GCGAACTTAAACCAAGTCTGAAAGAAAGAAATTAACCATCTTGAAGATTTGCGC 2220  
QY 2221 AGCATCTTAAACCAAGGCACTCTCTAGGCGCCCTGCTCTCAATGATGATGATGATGAT 2280  
Db 2221 AGCATCTTAAACCAAGGCACTCTCTAGGCGCCCTGCTCTCAATGATGATGATGATGAT 2280  
QY 2281 CCCCCAAGCCGAGATCTTCAAGGCTCTCTCTCATGATGATGATGATGATGATGATGAT 2340  
Db 2281 CCCCCAAGCCGAGATCTTCAAGGCTCTCTCTCATGATGATGATGATGATGATGATGAT 2340  
QY 2341 GCTTGCTTCCCGTAAATGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 2400  
Db 2341 GCTTGCTTCCCGTAAATGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 2400



QY 2401 CCAGAAAGAAATGAGAGGAGAACTAGTCTAAGAGAAATCTGAGGGAGCAAGTGTTC 2460  
Db 2401 CCAGAAAGAAATGAGAGGAGAACTAGTCTAAGAGAAATCTGAGGGAGCAAGTGTTC 2460  
QY 2461 CTCAGAGGAGAAAGGGGCTCCAGCTCCAGAGAAATTCAGAGAGTGGGACCTGCAAGAG 2520  
Db 2461 CTCAGAGGAGAAAGGGGCTCCAGCTCCAGAGAAATTCAGAGAGTGGGACCTGCAAGAG 2520  
QY 2521 TGGGAGCGCTGGGGCTGAGCGGGGCTGAAAGGAGAGAGTAAAGGAGGAGCAAGCTGAA 2580  
Db 2521 TGGGAGCGCTGGGGCTGAGCGGGGCTGAAAGGAGAGAGTAAAGGAGGAGCAAGCTGAA 2580  
QY 2581 GCTGCCAGATGTTCACTGTTGTTCAAGGGGCTGGAGATTTCCGTTCCCTGTAAC 2640  
Db 2581 GCTGCCAGATGTTCACTGTTGTTCAAGGGGCTGGAGATTTCCGTTCCCTGTAAC 2640  
QY 2641 CTTTATCTTTCTCTGCTTGAAGAGAGAAAGTCTATTCATGAAAGGAGTCAAGTTTC 2700  
Db 2641 CTTTATCTTTCTCTGCTTGAAGAGAGAAAGTCTATTCATGAAAGGAGTCAAGTTTC 2700  
QY 2701 ATAAAGTCAAGTGTAAATTCAGAGGCTGTGATGGATTTCCCTTCAGAGAGCCCTTAT 2760  
Db 2701 ATAAAGTCAAGTGTAAATTCAGAGGCTGTGATGGATTTCCCTTCAGAGAGCCCTTAT 2760  
QY 2761 TTAATGGGAATATGAGAGGAGAGTCTATTCCTAGAGCCCTTATTCAGAGAGAGTAC 2820  
Db 2761 TTAATGGGAATATGAGAGGAGAGTCTATTCCTAGAGCCCTTATTCAGAGAGAGTAC 2820  
QY 2821 TGAGTCTTTTCTTCTGCTTGTGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880  
Db 2821 TGAGTCTTTTCTTCTGCTTGTGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880  
QY 2881 TGAGAGCGGTGAGAAACCTTGAGATCAGAGAGTGGTTTCTTTCTGTTCTGCTAT 2940  
Db 2881 TGAGAGCGGTGAGAAACCTTGAGATCAGAGAGTGGTTTCTTTCTGTTCTGCTAT 2940  
QY 2941 GGTGGCTGTGCGAGCGGTGGGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000  
Db 2941 GGTGGCTGTGCGAGCGGTGGGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000  
QY 3001 ATAAAGACCCCTTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060  
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QY 3061 GGAATGTTGAGAGGGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 3120  
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Db 3121 GGACAGAGAGGAGGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180  
QY 3181 CAGAGCCGAGAGCCAAATGCTTCAAGAAAGCTCAATGAACCCAAAGCCCACTTTTCT 3240  
Db 3181 CAGAGCCGAGAGCCAAATGCTTCAAGAAAGCTCAATGAACCCAAAGCCCACTTTTCT 3240  
QY 3241 TCCCTAAGCATAGACATGCTTGGCATTAACCAAAAGAAATGAGAGTCAATGCT 3300  
Db 3241 TCCCTAAGCATAGACATGCTTGGCATTAACCAAAAGAAATGAGAGTCAATGCT 3300  
QY 3301 GGTAGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360  
Db 3301 GGTAGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360  
QY 3361 TTAATCTTTTCAAGCTTCAAGAGCCCAAGCAAGTCAAGAGTCAAGAGTCAAGAG 3420  
Db 3361 TTAATCTTTTCAAGCTTCAAGAGCCCAAGCAAGTCAAGAGTCAAGAGTCAAGAG 3420  
QY 3421 AGTGAAGTGAAG 3480  
Db 3421 AGTGAAGTGAAG 3480  
QY 3481 ACAAGTATTCAG 3540

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Db 3541 GTTCTAG 3600  
QY 3601 CCGATTTCTAATCTAATTTTCTTCTTCAAGCTGAGTAAATTCAGAGAGTCAAG 3660  
Db 3601 CCGATTTCTAATCTAATTTTCTTCTTCAAGCTGAGTAAATTCAGAGAGTCAAG 3660  
QY 3661 GTAGTAACTGAGCTGAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720  
Db 3661 GTAGTAACTGAGCTGAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720  
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Db 3721 GGAATTAGCAGCAG 3780  
QY 3781 TAAAGCCAAACAGATTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840  
Db 3781 TAAAGCCAAACAGATTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840  
QY 3841 CATTGAGAGATGTTACTATCTGATTCAGAAATGAGAGTGAACCTTTGCTGAGCTG 3900  
Db 3841 CATTGAGAGATGTTACTATCTGATTCAGAAATGAGAGTGAACCTTTGCTGAGCTG 3900  
QY 3901 TAAACAAACAGAGTGTAAATGCTCAAGTTCAGAGTAACTGAGAGAGAGAGAGAGAG 3959  
Db 3901 TAAACAAACAGAGTGTAAATGCTCAAGTTCAGAGTAACTGAGAGAGAGAGAGAGAG 3960  
QY 3960 AAGATGATCTTTAG 4019  
Db 3961 AAGATGATCTTTAG 4019  
QY 4020 CAGTTGGAATATTTACTTCAAGATTTGACAGTGTGTTGATTAACAACATTAAG 4079  
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QY 4080 TTGCTCAAAGCAATCTATTTCAGAGTGGCTTAAAGTACTTCTGACAGTTTGGTATA 4139  
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Db 4140 TTTATGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4199  
QY 4200 GGAATTTAACCTTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4259  
Db 4200 GGAATTTAACCTTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4259  
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QY 4320 ACTCAAGGTGATTAACAGTACCTGATTTTGTCAATTAACCAATGAATCAAGACAT 4379  
Db 4320 ACTCAAGGTGATTAACAGTACCTGATTTTGTCAATTAACCAATGAATCAAGACAT 4379  
QY 4380 TTTATCTAATTTAAGTGTGAGATAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4439  
Db 4380 TTTATCTAATTTAAGTGTGAGATAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4439  
QY 4440 ACTTGAATTTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4499  
Db 4440 ACTTGAATTTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4499  
QY 4500 AATTTGAATTTTGAATCAATTTCAATTAATTTGTTTCTTGTGATCTAATTT 4559  
Db 4500 AATTTGAATTTTGAATCAATTTCAATTAATTTGTTTCTTGTGATCTAATTT 4559  
QY 4560 TATATTTGAAACATCTTTGAGAGAGTCCCAATTTCAACCAATGAGTCTCTG 4619







```

QY      1493  CCCACCTCAGCCTCTCTAAGTGTGGATTACAGGATGATGACCGCGCCGCCAA 1550
Db      350  CCCACCTCGGCGCTCCCAAGTGTGGATTACAGGATGACCGATGCGCTGGCCAA 467

RESULT 14
US-09-801-861-3/c
; Sequence 3, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Human
US-09-801-861-3

Query Match      3.4%; Score 176.8; DB 4; Length 53332;
Best Local Similarity 79.0%; Pred. No. 2.1e-33;
Matches 226; Conservative 0; Mismatches 52; Indels 8; Gaps 1;

QY      1290  TGTGTCTTACACCTACCTGATAGCTCTCTACACCTGAGCTCACTGCACTCTGCTCC 1349
Db      46722  TGTGTCTCAGCTGAGTGCATGTCAGATCTCTCTCATCTGCACTCTCTCTCT 46663
QY      1350  AGGTTCAAGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1408
Db      46662  GGGTTCAAGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 46603
QY      1409  -----CGGCTATTTTGTATTTGTATTTAGTAGAGATGGGGTTTACCATTTAGCCCGGC 1461
Db      46602  CCACGTTGCGCTATTTTGTATTTAGTAGAGATGGGGTTTACCATTTAGCCAGGC 46543
QY      1462  TGTCTTGAACCTCTGACCTGAGTGATCCACCACCTCACTCTCTAAGTCTGGGAT 1521
Db      46542  TGTCTTGAACCTCTGAGTGAAGTATCCACCACCTGCGCTCCCAAGTCTGGGAT 46483
QY      1572  TACAGGCATGATGATACCGCGCGCCGCCAAGGTCAGTGTATTAA 1567
Db      46482  TACAGGCATGAGCCACTGCGGCCCGGCGCAATCTGTCTTTATAA 46437

RESULT 15
US-09-539-333D-37/c
; Sequence 37, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bouguetelret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essiloux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14

; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 37
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: 5'UTR
; LOCATION: 1..719
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 720..1118
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1119..1154
; FEATURE:
; NAME/KEY: polyA.signal
; LOCATION: 1131..1136
; FEATURE:
; NAME/KEY: allele
; LOCATION: 191
; OTHER INFORMATION: 8-121-187 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 313
; OTHER INFORMATION: 8-122-271 : deletion of CAA
; FEATURE:
; NAME/KEY: allele
; LOCATION: 314
; OTHER INFORMATION: 8-122-272 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 368
; OTHER INFORMATION: 8-122-326 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 390
; OTHER INFORMATION: 8-123-55 : polymorphic base A or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 814
; OTHER INFORMATION: 8-128-61 : polymorphic base G or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 822
; OTHER INFORMATION: 8-128-69 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 838
; OTHER INFORMATION: 8-128-85 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 897
; OTHER INFORMATION: 8-129-50 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 908
; OTHER INFORMATION: 8-129-60 : deletion of A
US-09-539-333D-37
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Query Match 3.4%; Score 176.6; DB 4; Length 1154;  
 Best Local Similarity 75.9%; Pred. No. 3.2e-34;  
 Matches 233; Conservative 1; Mismatches 65; Indels 8; Gaps 1;

QY	1253	CACGATGTTACAGCCAGAAAGCTCCGAGAGGTGAGAGTCTGTGTCTTACACCTACTGTGTA	1312
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QY	1313	TGCTTACACCTGAGCTCACTGCAACCTCTGCTCCAGGTTCAAGCAATTCTCTGTCT	1372
DB	760	GTGGTGTGATCTTGGCTCACTGCAACCTCGGCTCCAGGTTCAAGCAATTCTCTGTCT	701
QY	1373	CAGCCTCCCGGCTAGCTGGGACTACAGC-----GACCGCCGGCTAATTTTGTAT	1424
DB	700	CAGCCTCCCGGCTAGCTGGGACTACAGCAGCCTGCCACCATGCTGGCTAATTTTGTAT	641
QY	1425	TGTTAGTAGAGATGGGATTTTCAACATATTAGCCCGGCTGTCTTGAATCTCCGACTCAG	1484
DB	640	TTTTAGTAGAGATGGGATTTTCAACATATTGTCTGAGCTGTCTTGAATCTCCGACTCAG	581
QY	1485	GTGATCCACCACCTCAGCCTCTTAAAGTGTGGGATTAAGGCAATGACACCGCGCC	1544
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QY	1545	GGCCAAG 1551	
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Search completed: September 19, 2004, 21:35:25  
 Job time : 343 secs

100





Db 1921 TGGGTGCTCTGAGCAACCTGCGACCCGTCGCACTGGTGTGTTTGTATCACTCTCTAGG 1980  
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTGTTTCATTCATCCAGGCAATTCATGCAATT 2040  
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTGTTTCATTCATCCAGGCAATTCATGCAATT 2040  
Qy 2041 TATTGAGTACTTATATCTGCGACACACAGAGACAAATATGTGTAGCAAAAGCACTGCG 2100  
Db 2041 TATTGAGTACTTATATCTGCGACACACAGAGACAAATATGTGTAGCAAAAGCACTGCG 2100  
Qy 2101 CCTACCTTGTGAGAGTGAAGTTTCTCATGGAAGAGTGCAGAGAAATTAATAGCCA 2160  
Db 2101 CCTACCTTGTGAGAGTGAAGTTTCTCATGGAAGAGTGCAGAGAAATTAATAGCCA 2160  
Qy 2161 GCCAATTTAAACCAAGTGTGAAGAAAGAAATTAACACCATCTTGAAGAAATGTGCGC 2220  
Db 2161 GCCAATTTAAACCAAGTGTGAAGAAAGAAATTAACACCATCTTGAAGAAATGTGCGC 2220  
Qy 2221 AGCATCCCTTAAACAAGGCACTGCTAGAGCCCGCTGCTGCTCATGTCGCGGAGG 2280  
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Qy 2281 CCCCCAAGCCGAGTCTTCAAGCCTCTCTCATCATGTCAGAGCGTGCAGCTGGCT 2340  
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Qy 2341 GCTGCGCTTCCGCTGAATCGTCTGTGTGATCTGAGCTGAGAGCTCTTGGCTCCAGGCT 2400  
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Qy 2401 CCAGAAAGGAAATGAGAGAGGAACTAGTCTTAACGAGAACTGTGAAGGAGACAGTCTTC 2460  
Db 2401 CCAGAAAGGAAATGAGAGAGGAACTAGTCTTAACGAGAACTGTGAAGGAGACAGTCTTC 2460  
Qy 2461 CTCAGAGGAAAGAGGAGCTCCAGCTCCAGAGAAATTCAGAGAGTGTGGAGATGCGAGGAG 2520  
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Qy 2641 CTTTATCTTTCTCTGCTTGAAGAGAAAGTCTATTCATGAAGGATGCACTTTC 2700  
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Qy 2701 AATAAGTACGCTGTAAATTCAGAGGCTGTGAAGGCTGTGAGTGTCTTCTTCAAGAGCTTAT 2760  
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Qy 2761 TTAATGGAATATAGAGAGCGAGTCAATTCAGGCGGTTAATTCAGCGAAAGATGAC 2820  
Db 2761 TTAATGGAATATAGAGAGCGAGTCAATTCAGGCGGTTAATTCAGCGAAAGATGAC 2820  
Qy 2821 TGGAGTCTTTTCTTCAAGTCTTCTGAGCAACTATCAAGCCGTTGAGTGTGAGCTTGA 2880  
Db 2821 TGGAGTCTTTTCTTCAAGTCTTCTGAGCAACTATCAAGCCGTTGAGTGTGAGCTTGA 2880  
Qy 2881 TGCAGAGCGTGCAGAAACCTTGAATCAGAGAGACTCGTCTTCTTCTGAGCTTGA 2940  
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Db 3061 GATGTTTGAAGAGGAGAGGAGAGAGTGTGAGAGAGTGTGAGAGGAGAGGAGG 3120  
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Db 3121 GAGCAGAGAGGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 3180  
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Db 3181 CAGAGCCGAGAGCCAAATGCTTCAAGAAAGCTCAATGAAGCCCAAGCCCAATTTCT 3240  
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Db 3241 TCCCTAAGCATAGCAATGAGCAATTTGCCAATTAACCAAAAGATGAGAGACTTACTG 3300  
Qy 3301 GGTAGCTTTTGTGCTGCAATTAAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 3360  
Db 3301 GGTAGCTTTTGTGCTGCAATTAAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 3360  
Qy 3361 TTAAGCTTTTCACTTGAACAGACCCCAAGCTGAGAGTGTGAGAGAGTGTGAGAG 3420  
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Db 3481 ACAGATTCATTAAG 3540  
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Db 3601 CTTGATTTCTAATTAATTAATTTTCTTTTACAGCTGATTAATCTGAGAGTCAAG 3660  
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Qy 3901 TAAAGCAAG 3960  
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[illegible]

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AAAS7486			
ID	AAAS7486	standard; DNA; 6169 BP.	
XX			
AC	AAAS7486;		
XX			
XX	20-OCT-2000	(first entry)	
DT			
XX			
DE	A TIGR (trabecular meshwork inducible glucocorticoid receptor) promoter.		
XX			
DE	TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;		
KM	glaucoma; steroid sensitivity; progressive ocular hypertension;		
KW	vision loss; ss.		
XX			
OS	Homo sapiens.		
XX			
XX			
FH	Key	Location/Qualifiers	
FT	mutation	replace(4256, G)	
FT		/*tag= d	
FT		/note= "TIGRmt4 mutant"	
FT	mutation	replace(4337, G)	
FT		/*tag= a	
FT		/note= "TIGRmt1 mutant"	
FT	mutation	replace(4950, T)	
FT		/*tag= b	
FT		/note= "TIGRmt2 mutant"	
FT	mutation	4998	
FT		/*tag= c	
FT		/note= "GRT added to produce TIGRmt3 mutant"	
FT	mutation	replace(5113, C)	
FT		/*tag= e	
FT		/note= "TIGRmt11 mutant"	
XX			
PN	WO200042220-A1.		
XX			
PD	20-JUL-2000.		
XX			
PF	11-JAN-2000; 2000WO-US000559.		
XX			
PR	11-JAN-1999; 99US-00227881.		
PR	07-MAY-1999; 99US-00306828.		
PA	(REGC ) UNIV CALIFORNIA.		
XX			
XX	Nguyen TD, Polansky JR, Chen P, Chen H;		
PI	WPI; 2000-491060/43.		
DR			
XX			
XX			
PT	Diagnosis, prognosis and treatment of glaucoma, based on detecting		
PT	specific polymorphisms in the promoter of the trabecular meshwork		
PT	inducible glucocorticoid receptor gene.		
XX			
PS	Claim 37; Page 105-107; 122pp; English.		
XX			
CC	The present sequence represents a TIGR (trabecular meshwork inducible		
CC	glucocorticoid receptor) promoter. The specification describes a method		
CC	for the diagnosis, prognosis and treatment of glaucoma, based on		
CC	detecting specific polymorphisms in the promoter of the TIGR gene. The		
CC	method is used for diagnosis and prognosis of glaucoma (of all types),		
CC	steroid sensitivity and progressive ocular hypertension that leads to		
CC	loss of vision. Glaucoma can be treated by administering an agent that		
CC	binds to cis-acting elements within the TIGR promoter. The TIGR promoter		
CC	(or other regulatory regions) can be used to express homologous or		
CC	heterologous genes, particularly for treating glaucoma, also to generate transgenic		
CC	therapeutic transgenes for treating glaucoma, also to generate transgenic		
CC	animals and in screening for compounds (specific modulators) with		
CC	diagnostic or therapeutic potential. Fragments of the TIGR sequence can		
CC	be used as amplification primers or probes, e.g. for isolating related		
CC	sequences in non-human animals		

Mon Sep 20 15:02:13 2004

us-09-227-881-34.rng

Page 5

XX	Sequence 6169 BP, 1702 A, 1389 C, 1491 G, 1587 T, 0 U, 0 Other;	
SQ	Query Match	100.0%; Score 5271; DB 3; Length 6169;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 5271; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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DB	1 ATCTTTGTCAGTTTACCTCAGGCTATTAAGAATGAATGATTAACCAATGTGAAG	60
QY	1 TCCTATAACTGTATAGCTCCATTCGATGTATGTCTTGGAGAGATGATAAATCA	120
DB	1 TCCTATAACTGTATAGCTCCATTCGATGTATGTCTTGGAGAGATGATAAATCA	120
QY	61 TCCTATAACTGTATAGCTCCATTCGATGTATGTCTTGGAGAGATGATAAATCA	120
DB	61 TCCTATAACTGTATAGCTCCATTCGATGTATGTCTTGGAGAGATGATAAATCA	120
QY	121 GGAAGAGAGATATCCAGCTTACGCAAGTGTCCAGGCTGTCTCTTATTTTATGA	180
DB	121 GGAAGAGAGATATCCAGCTTACGCAAGTGTCCAGGCTGTCTCTTATTTTATGA	180
QY	181 CAGATGTCTCTCCGACGAGAGATATCTTCAGAGAAATCCATCAATGATGTAATC	240
DB	181 CAGATGTCTCTCCGACGAGAGATATCTTCAGAGAAATCCATCAATGATGTAATC	240
QY	241 CATCAACAGAGAGCTTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGAAATGCGAG	300
DB	241 CATCAACAGAGAGCTTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGAAATGCGAG	300
QY	301 GAGAGCAATATATGATGAAAAATTAATCTTCCCTTTGTTTAAATTTAGAAAAAATG	360
DB	301 GAGAGCAATATATGATGAAAAATTAATCTTCCCTTTGTTTAAATTTAGAAAAAATG	360
QY	361 ATAGAGACCAAAATCAATGATTAAGAAAAACAGCTCAGAAAAAAGATGTTTCCAATTGG	420
DB	361 ATAGAGACCAAAATCAATGATTAAGAAAAACAGCTCAGAAAAAAGATGTTTCCAATTGG	420
QY	421 TAAATTAAGTATTTGTTCTTGGGAGAGAGACTCCATGTGATGCTTATGAGAAATGGGA	480
DB	421 TAAATTAAGTATTTGTTCTTGGGAGAGAGACTCCATGTGATGCTTATGAGAAATGGGA	480
QY	481 AAAGCTCAAAAGCATGATGATCCAGATCCCAAGTGAATTAATTTTAAAAACAGAT	540
DB	481 AAAGCTCAAAAGCATGATGATCCAGATCCCAAGTGAATTAATTTTAAAAACAGAT	540
QY	541 GGCACTACTCTGGGAGAGCAAGTTCAGAAAGTTCATGTTAGCAAGAGATTAACAATAC	600
DB	541 GGCACTACTCTGGGAGAGCAAGTTCAGAAAGTTCATGTTAGCAAGAGATTAACAATAC	600
QY	601 AGCAAAATCAAAATTTCCGCAAAATGCAAGAGAAATGGGGAATGGGAAAGCTTTATAC	660
DB	601 AGCAAAATCAAAATTTCCGCAAAATGCAAGAGAAATGGGGAATGGGAAAGCTTTATAC	660
QY	661 AGTATTAAGGCAAGTTCATGTTTGGCAACCTCCCTCTTATACAGGAAACCAAA	720
DB	661 AGTATTAAGGCAAGTTCATGTTTGGCAACCTCCCTCTTATACAGGAAACCAAA	720
QY	721 ATTGACTGGGCTAAGGCTGAGCTTCAAGGGAATTAAGAAAAATGAGAGCAAAACAAA	780
DB	721 ATTGACTGGGCTAAGGCTGAGCTTCAAGGGAATTAAGAAAAATGAGAGCAAAACAAA	780
QY	781 GACATGTTAAAGGCAACCAAGATTTGAGGCTTCAAGAGAGAGTGGCCCTCAGCA	840
DB	781 GACATGTTAAAGGCAACCAAGATTTGAGGCTTCAAGAGAGAGTGGCCCTCAGCA	840
QY	841 GGGAGCCCTGAGGCAATTTGGCTTTAGAGAGGCTTTCTTAAGAGATTTTAAGAAATC	900
DB	841 GGGAGCCCTGAGGCAATTTGGCTTTAGAGAGGCTTTCTTAAGAGATTTTAAGAAATC	900
QY	901 TTGAAGATCATGAAATTTTAACATTTTAAGTAAACAAATATGCGATGATATGAG	960
DB	901 TTGAAGATCATGAAATTTTAACATTTTAAGTAAACAAATATGCGATGATATGAG	960
QY	961 TTGAAGATCATGAAATTTTAAGTAAAGTCAAGGATTAAGATGATGATGATGATGATG	1020
DB	961 TTGAAGATCATGAAATTTTAAGTAAAGTCAAGGATTAAGATGATGATGATGATGATG	1020
QY	1021 GATAGGTCAGAAATCATTAAGAAATCACTGTGTCCATCTTAATTTTCAAGAAATGATC	1080
DB	1021 GATAGGTCAGAAATCATTAAGAAATCACTGTGTCCATCTTAATTTTCAAGAAATGATC	1080
QY	1081 TGTATAGGCTTCACACAGAGCCGATGTGTGACCTTAACCAATCAACCAACCA	1140
DB	1081 TGTATAGGCTTCACACAGAGCCGATGTGTGACCTTAACCAATCAACCAACCA	1140
QY	1141 GTGGCTCAACATTTTAAAGCTGATCACTGATGATGATGATGATGATGATGATGATG	1200
DB	1141 GTGGCTCAACATTTTAAAGCTGATCACTGATGATGATGATGATGATGATGATGATG	1200
QY	1201 TGTGAGCCCATCCGCTCCACAGAAATGTCCCACTTGAATTTTGTGATGATGATG	1260
DB	1201 TGTGAGCCCATCCGCTCCACAGAAATGTCCCACTTGAATTTTGTGATGATGATGATG	1260
QY	1261 TACAGCAGAAAGCTCCGAGAGGTGAGAGGTGTGTGATGATGATGATGATGATGATG	1320
DB	1261 TACAGCAGAAAGCTCCGAGAGGTGAGAGGTGTGTGATGATGATGATGATGATGATG	1320
QY	1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGAGTTCAGCAATTTCTCTGCTCAGGCTCC	1380
DB	1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGAGTTCAGCAATTTCTCTGCTCAGGCTCC	1380
QY	1381 CGGTAGCTGGGACATACAGAGGCAAGCCCGCTAATTTTGTATGATGATGATGATG	1440
DB	1381 CGGTAGCTGGGACATACAGAGGCAAGCCCGCTAATTTTGTATGATGATGATGATGATG	1440
QY	1441 GTTACACATATTAACCCGCTGTGAACTCTGATCACTGATGATGATGATGATGATG	1500
DB	1441 GTTACACATATTAACCCGCTGTGAACTCTGATCACTGATGATGATGATGATGATG	1500
QY	1501 AGCTCTTAAGTGTGGGATTAAGAGATGATGATGATGATGATGATGATGATGATG	1560
DB	1501 AGCTCTTAAGTGTGGGATTAAGAGATGATGATGATGATGATGATGATGATGATG	1560
QY	1561 TTAATTAAGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1620
DB	1561 TTAATTAAGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1620
QY	1621 TAAATTAAGGATTTTGGGATGATGATGATGATGATGATGATGATGATGATGATG	1680
DB	1621 TAAATTAAGGATTTTGGGATGATGATGATGATGATGATGATGATGATGATGATG	1680
QY	1681 CACTGCTCTATCACTTCTTCCCTCATCTTCACTTCACTTCACTTCACTTCACTT	1740
DB	1681 CACTGCTCTATCACTTCTTCCCTCATCTTCACTTCACTTCACTTCACTTCACTT	1740
QY	1741 CACATGCTTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1800
DB	1741 CACATGCTTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1800
QY	1801 TTCCATTTGGGCACTGT	1860
DB	1801 TTCCATTTGGGCACTGT	1860
QY	1861 TGAAGCCCCCGAGAGGTTTCTCTCAGTGGGAGAGGCTGCAAGCAAGCCGAGGCTC	1920
DB	1861 TGAAGCCCCCGAGAGGTTTCTCTCAGTGGGAGAGGCTGCAAGCAAGCCGAGGCTC	1920
QY	1921 TGGGCTGCTGAGCACTGCAAGCCGCTGCAAGCCGCTGCAAGCCGCTGCAAGCCG	1980
DB	1921 TGGGCTGCTGAGCACTGCAAGCCGCTGCAAGCCGCTGCAAGCCGCTGCAAGCCG	1980
QY	1981 GACCTGTGCTTTCAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2040
DB	1981 GACCTGTGCTTTCAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2040
QY	2041 TATTAAGTATTAATTTGAGCAACAGAGCAAAATGATGATGATGATGATGATGATGATG	2100
DB	2041 TATTAAGTATTAATTTGAGCAACAGAGCAAAATGATGATGATGATGATGATGATGATG	2100

QY 2101 CCTACCTTGGTGGAGGTGACAGTTTCTCATGGAAGCGTGAGAAAGAAAATTATATAGCCA 2160  
Db 2101 CCTACCTTGGTGGAGGTGACAGTTTCTCATGGAAGCGTGAGAAAGAAAATTATATAGCCA 2160  
QY 2161 GCCAACTTAAACCCAGGTGTAAGAGAAAGAAATAAACCACTCTGTAAGAAATTTGTGGC 2220  
Db 2161 GCCAACTTAAACCCAGGTGTAAGAGAAAGAAATAAACCACTCTGTAAGAAATTTGTGGC 2220  
QY 2221 AGCATCCCTTAAACAGGCACTCCCTAGAGCCGCCCTGCTGCTCATCTGTGCCGAGG 2280  
Db 2221 AGCATCCCTTAAACAGGCACTCCCTAGAGCCGCCCTGCTGCTCATCTGTGCCGAGG 2280  
QY 2281 CCCCAGAGCCGAGTCTTCAAGCCCTCCCTCATAGTCAAGCGTGTGAGCTGAGCTGAGCT 2340  
Db 2281 CCCCAGAGCCGAGTCTTCAAGCCCTCCCTCATAGTCAAGCGTGTGAGCTGAGCTGAGCT 2340  
QY 2341 GCTGCTTCCCGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400  
Db 2341 GCTGCTTCCCGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400  
QY 2401 CCGAAGAAAGAAATGAGAGGAGAACTAGTCTAACGGAATCTGAGAGGAGCAAGTCTTTC 2460  
Db 2401 CCGAAGAAAGAAATGAGAGGAGAACTAGTCTAACGGAATCTGAGAGGAGCAAGTCTTTC 2460  
QY 2461 CTGAGAGGAGAGGAGGCTCAAGTCTCAAGAGAAATTCAGAGAGTGGGAGCTGAGAGGAG 2520  
Db 2461 CTGAGAGGAGAGGAGGCTCAAGTCTCAAGAGAAATTCAGAGAGTGGGAGCTGAGAGGAG 2520  
QY 2521 TGGGAGCGCTGGGCTGAGCGGCTGTGAAGCGAGAAAGGTGAAAGGAGGAGGCTGAA 2580  
Db 2521 TGGGAGCGCTGGGCTGAGCGGCTGTGAAGCGAGAAAGGTGAAAGGAGGAGGCTGAA 2580  
QY 2581 GCTGCCAGATGTTCAAGTGTGTGACAGGAGGAGTTCCTGCTGCTGCTGCTGCTGCTGAGC 2640  
Db 2581 GCTGCCAGATGTTCAAGTGTGTGACAGGAGGAGTTCCTGCTGCTGCTGCTGCTGCTGAGC 2640  
QY 2641 CTTTTCCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
Db 2641 CTTTTCCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
QY 2701 ATTAAGTCAAGCTTAATAATTCAGAGGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTTAT 2760  
Db 2701 ATTAAGTCAAGCTTAATAATTCAGAGGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTTAT 2760  
QY 2761 TTAATGGAAATTAAGAGAGAGCTCATTTCTAGGCGTAAATTCAGAGAGAGTGAAC 2820  
Db 2761 TTAATGGAAATTAAGAGAGAGCTCATTTCTAGGCGTAAATTCAGAGAGAGTGAAC 2820  
QY 2821 TGGAGTCTTCTCTCATGCTCTTCTGAGCACTCATAGCCCTGTGTGAGACTTGTCTTA 2880  
Db 2821 TGGAGTCTTCTCTCATGCTCTTCTGAGCACTCATAGCCCTGTGTGAGACTTGTCTTA 2880  
QY 2881 TGCAGAGCGTGAAGAACTTGAATCAGAGACTCGGTTTTCTTCTGCTGCTGCTGCTTAT 2940  
Db 2881 TGCAGAGCGTGAAGAACTTGAATCAGAGACTCGGTTTTCTTCTGCTGCTGCTGCTTAT 2940  
QY 2941 GGTGGCTGTGAGACCTGTGGGAAAGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 3000  
Db 2941 GGTGGCTGTGAGACCTGTGGGAAAGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 3000  
QY 3001 ATTAAGACCTTGAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060  
Db 3001 ATTAAGACCTTGAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060  
QY 3061 GATGTTGAGAGGAG 3120  
Db 3061 GATGTTGAG 3120  
QY 3121 GGAAG 3180  
Db 3121 GGAAG 3180

QY 3181 CAGAGCCGAGAGCCCAATGCTTTCAGAGAAAGTCAATGAAACCCCAAGCCATTTTCT 3240  
Db 3181 CAGAGCCGAGAGCCCAATGCTTTCAGAGAAAGTCAATGAAACCCCAAGCCATTTTCT 3240  
QY 3241 TCCCTAAGATGAGCAATGGCTTTTCCCATTAACCAAAAGATGCAAGACTTAAGTGT 3300  
Db 3241 TCCCTAAGATGAGCAATGGCTTTTCCCATTAACCAAAAGATGCAAGACTTAAGTGT 3300  
QY 3301 GGTAGCTTTTGGCTGCAATCAAAAATGCGGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 3360  
Db 3301 GGTAGCTTTTGGCTGCAATCAAAAATGCGGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 3360  
QY 3361 TTAACCTTTTCACTGACCAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420  
Db 3361 TTAACCTTTTCACTGACCAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420  
QY 3421 AGTACCTGACAGGAG 3480  
Db 3421 AGTACCTGACAGGAG 3480  
QY 3481 ACAGATTAATTAAG 3540  
Db 3481 ACAGATTAATTAAG 3540  
QY 3541 GTTCTAG 3600  
Db 3541 GTTCTAG 3600  
QY 3601 CTTGATTTCTAATCTAATTTTCTTTCCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3660  
Db 3601 CTTGATTTCTAATCTAATTTTCTTTCCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3660  
QY 3661 GATGATTAAG 3720  
Db 3661 GATGATTAAG 3720  
QY 3721 GAGATGAG 3780  
Db 3721 GAGATGAG 3780  
QY 3781 TAAAGCCAAACAGATTAAG 3840  
Db 3781 TAAAGCCAAACAGATTAAG 3840  
QY 3841 CATTCAG 3900  
Db 3841 CATTCAG 3900  
QY 3901 TAAACAAACCCAGATTAAG 3960  
Db 3901 TAAACAAACCCAGATTAAG 3960  
QY 3961 AGATTAAGATCTTAAG 4020  
Db 3961 AGATTAAGATCTTAAG 4020  
QY 4021 AGTTGAGAAATTTTCACTTCAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4080  
Db 4021 AGTTGAGAAATTTTCACTTCAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4080  
QY 4081 TGCCTAAG 4140  
Db 4081 TGCCTAAG 4140  
QY 4141 TTAATGCTAATGCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTT 4200  
Db 4141 TTAATGCTAATGCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTT 4200  
QY 4201 GATTAATTAACCTAAG 4260  
Db 4201 GATTAATTAACCTAAG 4260  
QY 4261 TGTTTTACACCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4320

[illegible]

XX		
PT	20-OCT-2000	(first entry)
DE	A TIGR (trabecular meshwork inducible glucocorticoid receptor) promoter.	
XX		
KW	TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;	
KM	glaucoma; steroid sensitivity; progressive ocular hypertension;	
KW	vision loss; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	mutation	/replace(4256, G)
FT		/tag= d
FT		/note= "TIGRmt4 mutant"
FT	mutation	/replace(4337, G)
FT		/tag= a
FT		/note= "TIGRmt1 mutant"
FT	mutation	/replace(4950, T)
FT		/tag= b
FT		/note= "TIGRmt2 mutant"
FT	mutation	/tag= c
FT		/note= "TIGR added to produce TIGRmt3 mutant"
FT	mutation	/replace(5113, C)
FT		/tag= e
FT		/note= "TIGRmt11 mutant"
XX		
PN	WO200042220-A1.	
PD	20-JUL-2000.	
XX		
PP	11-JAN-2000; 2000MO-US000559.	
XX		
PR	11-JAN-1999; 99US-00227881.	
XX	07-MAY-1999; 99US-00306828.	
PA	(REGC ) UNIV CALIFORNIA.	
PI	Nguyen TD, Polansky JF, Chen P, Chen H;	
XX	WPI; 2000-491060/43.	
PT	Dagnosis, prognosis and treatment of glaucoma, based on detecting	
PT	inducible polymorphisms in the promoter of the trabecular meshwork	
PT	inducible glucocorticoid receptor gene.	
PS	Claim 79; Page 117-119; 123pp; English.	
XX		
CC	The present sequence represents a TIGR (trabecular meshwork inducible	
CC	glucocorticoid receptor) promoter. Isolated from an individual without	
CC	glaucoma. The specification describes a method for the diagnosis,	
CC	prognosis and treatment of glaucoma, based on detecting specific	
CC	polymorphisms in the promoter of the TIGR gene. The method is used for	
CC	diagnosis and prognosis of glaucoma (of all types), steroid sensitivity	
CC	and progressive ocular hypertension that leads to loss of vision.	
CC	Glaucoma can be treated by administering an agent that binds to cis-	
CC	acting elements within the TIGR promoter. The TIGR promoter (or other	
CC	regulatory regions) can be used to express homologous or heterologous	
CC	genes, particularly for tissue-specific expression of therapeutic	
CC	transgenes for treating glaucoma, also to generate transgenic animals and	
CC	in screening for compounds (specific modulators) with diagnostic or	
CC	therapeutic potential. Fragments of the TIGR sequence can be used as	
CC	amplification primers or probes, e.g. for isolating related sequences in	
CC	non-human animals	
XX		
Sequence	5271 BP; 1476 A; 1138 C; 1231 G; 1426 T; 0 U; 0 Other;	

RESULT 3
AAA57511
ID AAA57511 standard; DNA; 5271 BP
XX
AC AAA57511;

1 ATCTTGTTCAGTTTACCTCAGGCTATATGAAGAATGAATGAGTAAACCATGTGAAG 60



Db	1	ATCTTTGTTCACTTACCTCAGGGCTTTTATGAAATGAAATAGATTAACCAATGTGAAG	60
QY	61	TCCTATAAAGCTGATAGCCCTCCATTCGGATGATGTCTTTGGCAGATGATMAAGATCA	120
Db	61	TCTATAAACTGTATACCTCCATTCGGATGATGTCTTTGGCAGATGATMAAGATCA	120
QY	121	GGAGGAAGGATATCCACCTTAGCAAGTGTCCAGGCTGTGTCTTATTTTAACTGA	180
Db	121	GGAGGAAGGATATCCACCTTAGCAAGTGTCCAGGCTGTGTCTTATTTTAACTGA	180
QY	181	CAGATGTTGCTCTGCAGAGAGCTATTTCTTCAGAAACATCAATCCATATGTTAATC	240
Db	181	CAGATGTTGCTCTGCAGAGAGCTATTTCTTCAGAAACATCAATCCATATGTTAATC	240
QY	241	CATCAAAACAGAGTAAAGAAACAGGAATGATGTGGCATTTGCCAGAAAAATGCGAG	300
Db	241	CATCAAAACAGAGTAAAGAAACAGGAATGATGTGGCATTTGCCAGAAAAATGCGAG	300
QY	301	GAGAGCAAAATATGATGAAAAATTAACCTTTCCCTTGTGTTTATTTCCAGAAAAATG	360
Db	301	GAGAGCAAAATATGATGAAAAATTAACCTTTCCCTTGTGTTTATTTCCAGAAAAATG	360
QY	361	ATGAGACCAAAATCAATGATATAGGAAAAAGCTCAGAAAAAAAGATGTTCCAAATTGG	420
Db	361	ATGAGACCAAAATCAATGATATAGGAAAAAGCTCAGAAAAAAAGATGTTCCAAATTGG	420
QY	421	TAATTAGTATTTTGTCCTTTGGGAGAGACCTCCCATGTGACCTGATGGGAAATGGGA	480
Db	421	TAATTAGTATTTTGTCCTTTGGGAGAGACCTCCCATGTGACCTGATGGGAAATGGGA	480
QY	481	AAACGTCAAAAGCATATCTGATCCAGATCCCAAGTGAATTTATTTTAAAAACAGAT	540
Db	481	AAACGTCAAAAGCATATCTGATCCAGATCCCAAGTGAATTTATTTTAAAAACAGAT	540
QY	541	GGATCACTCTGTGGGAGGGAAGTGTAGAGAGTCAATGTAGCAAAAGACATTAACAATAC	600
Db	541	GGATCACTCTGTGGGAGGGAAGTGTAGAGAGTCAATGTAGCAAAAGACATTAACAATAC	600
QY	601	AGCAAAATCAAAATTTCCGCAAAATGACAGAGGAAAAATGGGACTGGGAAACCTTCAATAC	660
Db	601	AGCAAAATCAAAATTTCCGCAAAATGACAGAGGAAAAATGGGACTGGGAAACCTTCAATAC	660
QY	661	AGGATTTAGGCAATTGACCATTTGTTCGAACACTCCCGTCTATACAGGGAACACAAA	720
Db	661	AGGATTTAGGCAATTGACCATTTGTTCGAACACTCCCGTCTATACAGGGAACACAAA	720
QY	721	ATTGACTGGGCTAGGCTGACCTTCCTCAAGGGAAATATGAAAACTGAGAGCAAAACAA	780
Db	721	ATTGACTGGGCTAGGCTGACCTTCCTCAAGGGAAATATGAAAACTGAGAGCAAAACAA	780
QY	781	GACATGTTTAAAGGCAACGACAGACATTTGTAGGCTTCAAGAGCAGTGTCCCTCAGCA	840
Db	781	GACATGTTTAAAGGCAACGACAGACATTTGTAGGCTTCAAGAGCAGTGTCCCTCAGCA	840
QY	841	GGGACCTTAGGCAATTTGCTTTAGAGGCACTTTTCTTAAGGAATCTTAAAGAACTC	900
Db	841	GGGACCTTAGGCAATTTGCTTTAGAGGCACTTTTCTTAAGGAATCTTAAAGAACTC	900
QY	901	TTGAAAGATCATGAATTTTAAACATTTTAATATATAAACAATATCGATCGATATCAG	960
Db	901	TTGAAAGATCATGAATTTTAAACATTTTAATATATAAACAATATCGATCGATATCAG	960
QY	961	TTTAGACATAGGCTCCCAATTTTATTAAGTCAGGCAATCAAGATTAACGTGTCCAGCTCC	1020
Db	961	TTTAGACATAGGCTCCCAATTTTATTAAGTCAGGCAATCAAGATTAACGTGTCCAGCTCC	1020
QY	1021	GGATAGTACAGAAATCATTAGAAATCACTGTGTCCCATCTTAACCTTTTCAGAAATGATC	1080
Db	1021	GGATAGTACAGAAATCATTAGAAATCACTGTGTCCCATCTTAACCTTTTCAGAAATGATC	1080
QY	1081	TGTCAATAGCCTTCAACAAGGCCGATGTGTGACCTTCAACCAACATCTAACCCCA	1140

Db	1081	TGTCAATAGCCCTCACACACAGGCCCGATGTCTGTGACCTTACCAACCATCTTACAAACCCAA	1140
Qy	1141	GTCCTCAACCAATTGTTAAGCTGTCACTCAGTAGAGTCCCAATTACAAATGCGACCTCC	1200
Db	1141	GTCCTCAACCAATTGTTAAGCTGTCACTCAGTAGAGTCCCAATTACAAATGCGACCTCC	1200
Qy	1201	TGTGAGCCCATCCCGCTCCACAGGAAGTCTCCCACTTGAACCTTGTGCATCCAGTGT	1260
Db	1201	TGTGAGCCCATCCCGCTCCACAGGAAGTCTCCCACTTGAACCTTGTGCATCCAGTGT	1260
Qy	1261	TACAGCCAGAAAGTCCGTGAGAGGTGTGTCTTACACTTACTGTATGCTGTAC	1320
Db	1261	TACAGCCAGAAAGTCCGTGAGAGGTGTGTCTTACACTTACTGTATGCTGTAC	1320
Qy	1321	ACCTGAGCTCACTGCAACTCTGCTCCAGAGTTCAAGCAATTCCTGTCTCAGCTCC	1380
Db	1321	ACCTGAGCTCACTGCAACTCTGCTCCAGAGTTCAAGCAATTCCTGTCTCAGCTCC	1380
Qy	1381	CGCGTAGTGGAGCTACAGCGCGACGCCGCTAATTTTGTATTTGTATAGAGAGGG	1440
Db	1381	CGCGTAGTGGAGCTACAGCGCGACGCCGCTAATTTTGTATTTGTATAGAGAGGG	1440
Qy	1441	GTTTCACCATTTAGCCCGGCTGCTCTTGAACCTCCTGACCTCAGTGTATCCACCACTC	1500
Db	1441	GTTTCACCATTTAGCCCGGCTGCTCTTGAACCTCCTGACCTCAGTGTATCCACCACTC	1500
Qy	1501	AGCCTCTCAAAAGTCTGGAGTTTAAAGCAATGAGTCAACCGGCCCGCAAGGCTAGTG	1560
Db	1501	AGCCTCTCAAAAGTCTGGAGTTTAAAGCAATGAGTCAACCGGCCCGCAAGGCTAGTG	1560
Qy	1561	TTAATTAAGGAATACTTGAATGTGTTTCTAAACCAACAGGGAACAGACAAAGCTGTGA	1620
Db	1561	TTAATTAAGGAATACTTGAATGTGTTTCTAAACCAACAGGGAACAGACAAAGCTGTGA	1620
Qy	1621	TAAATTCAGGGATCTTGGGATGGGGATGTGCCATGAGCTGCTGCTAGTCCAGAC	1680
Db	1621	TAAATTCAGGGATCTTGGGATGGGGATGTGCCATGAGCTGCTGCTAGTCCAGAC	1680
Qy	1681	CACGTGTCCTCATCATCTTCTCCCTCATCTCATATTTTCAAGCTTAAGTTACATTTTAT	1740
Db	1681	CACGTGTCCTCATCATCTTCTCCCTCATCTCATATTTTCAAGCTTAAGTTACATTTTAT	1740
Qy	1741	CACCATCTTTTGTGTAGCCTTCCACATGTTACTGAATTAAGATATACATTAACCTAG	1800
Db	1741	CACCATCTTTTGTGTAGCCTTCCACATGTTACTGAATTAAGATATACATTAACCTAG	1800
Qy	1801	TTTCATTTGGGGCATCTGTGTGTGTGTATAGGGGAGAGGGCATGCCCAAGACTCCT	1860
Db	1801	TTTCATTTGGGGCATCTGTGTGTGTGTATAGGGGAGAGGGCATGCCCAAGACTCCT	1860
Qy	1861	TGAAGCCCCCGGAGAGGTTTCTCTTCCAGCTGGGGAGCCTCTGACAGCACCGGGCTCC	1920
Db	1861	TGAAGCCCCCGGAGAGGTTTCTCTTCCAGCTGGGGAGCCTCTGACAGCACCGGGCTCC	1920
Qy	1921	TGGGTGTCTTGAGCAACCTGCCACGCCGTGCCACTGTGTTGTTATCACTCTTAGG	1980
Db	1921	TGGGTGTCTTGAGCAACCTGCCACGCCGTGCCACTGTGTTGTTATCACTCTTAGG	1980
Qy	1981	GACCTGTGCTTCTTCTATTTCTGTGTACTCGTTCACTTCAACAGGATCATTTGCAATT	2040
Db	1981	GACCTGTGCTTCTTCTATTTCTGTGTACTCGTTCACTTCAACAGGATCATTTGCAATT	2040
Qy	2041	TATTGAGTACTTATATCTGCCAGACACAGAGCAAAATGTGTAGCAAGAGTCACTGC	2100
Db	2041	TATTGAGTACTTATATCTGCCAGACACAGAGCAAAATGTGTAGCAAGAGTCACTGC	2100
Qy	2101	CGTACCTGTGGAGGTGACAGTTTCTATGGAAGAAGCTGCAAGAAATTAATTAAGCA	2160
Db	2101	CGTACCTGTGGAGGTGACAGTTTCTATGGAAGAAGCTGCAAGAAATTAATTAAGCA	2160
Qy	2161	GCCCACTTAAACCCAGTGTGTAAGAAAGAAATTAACACATCTTTGAAGATTGTGGC	2220
Db	2161	GCCCACTTAAACCCAGTGTGTAAGAAAGAAATTAACACATCTTTGAAGATTGTGGC	2220



QY 2221 AGCATCCCTTAACAAAGGCGACCTCCCTAGCGCCCTGCTGCTCATCTGCGGAGG 2280  
Db 2221 AGATCCCTTAACAAAGGCGACCTCCCTAGCGCCCTGCTGCTCATCTGCGGAGG 2280  
QY 2281 CCCCAGGCGCGAGTCTTCAAGCTCTCTCCATCAAGTCAAGCGCTGAGCTGCT 2340  
Db 2281 CCCCAGGCGCGAGTCTTCAAGCTCTCTCCATCAAGTCAAGCGCTGAGCTGCT 2340  
QY 2341 GCTGCTCTCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400  
Db 2341 GCTGCTCTCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400  
QY 2401 CCAAGAGGAAATGAGAGGAGAACTAGTCTAACGAGAAATCTGAGGAGGACAGTGTTC 2460  
Db 2401 CCAAGAGGAAATGAGAGGAGAACTAGTCTAACGAGAAATCTGAGGAGGACAGTGTTC 2460  
QY 2461 CTGAGAGGAGAAAGGCGCTTCCAGTCCAGAGAAATTCAGAGAGTGGGAGACTGACAGAG 2520  
Db 2461 CTGAGAGGAGAAAGGCGCTTCCAGTCCAGAGAAATTCAGAGAGTGGGAGACTGACAGAG 2520  
QY 2521 TGGGAGAGCTGGGAGTCTGAGGAGTCTGAGAAAGGAGAGTGAAGAGGAGGCTGAA 2580  
Db 2521 TGGGAGAGCTGGGAGTCTGAGGAGTCTGAGAAAGGAGAGTGAAGAGGAGGCTGAA 2580  
QY 2581 GCTGCCAGATGTTCAAGTGTGTTCAAGGAGGCTGGAGATTTCCGTTGCTTCTGTAGC 2640  
Db 2581 GCTGCCAGATGTTCAAGTGTGTTCAAGGAGGCTGGAGATTTCCGTTGCTTCTGTAGC 2640  
QY 2641 CTTTATATCTTTCTCTGCTTGGAGAGAGAAAGTCTATTTCAATGAAGGATGAGTTTC 2700  
Db 2641 CTTTATATCTTTCTCTGCTTGGAGAGAGAAAGTCTATTTCAATGAAGGATGAGTTTC 2700  
QY 2701 ATAAAGTCACTGTAAATTCAGAGGAGTGTGAGGATTTCTTCCATCAGAGGCTTTAT 2760  
Db 2701 ATAAAGTCACTGTAAATTCAGAGGAGTGTGAGGATTTCTTCCATCAGAGGCTTTAT 2760  
QY 2761 TTATATGGAAATATAGAGAGGAGTCAATTTCTAGGCGCTTAATTCAGAGAGAGTAC 2820  
Db 2761 TTATATGGAAATATAGAGAGGAGTCAATTTCTAGGCGCTTAATTCAGAGAGAGTAC 2820  
QY 2821 TGGAGTCTTTCTTCTGCTTGGAGAGAGTCAATTTCTAGGCGCTTAATTCAGAGAGAGTAC 2880  
Db 2821 TGGAGTCTTTCTTCTGCTTGGAGAGAGTCAATTTCTAGGCGCTTAATTCAGAGAGAGTAC 2880  
QY 2881 TGCAGAGCGTTCGAAAACCTTGAATCAGAGAGTGTGATTTCTTCTGCTTCTGCT 2940  
Db 2881 TGCAGAGCGTTCGAAAACCTTGAATCAGAGAGTGTGATTTCTTCTGCTTCTGCT 2940  
QY 2941 GGTGGCTGTGGAGCGGTGGAGAGTGTCTGCTTCCGCGGAGTACTGCTTCTGCT 3000  
Db 2941 GGTGGCTGTGGAGCGGTGGAGAGTGTCTGCTTCCGCGGAGTACTGCTTCTGCT 3000  
QY 3001 ATAAAGACCTTGAAGTCTGATGTCTGAGAACATTCCTGTGATTTCTGCTGAGGAG 3060  
Db 3001 ATAAAGACCTTGAAGTCTGATGTCTGAGAACATTCCTGTGATTTCTGCTGAGGAG 3060  
QY 3061 GGAATTTGAAGGAGAGAGAGAGTGTGAGAACATTCCTGTGATTTCTGCTGAGGAG 3120  
Db 3061 GGAATTTGAAGGAGAGAGAGAGTGTGAGAACATTCCTGTGATTTCTGCTGAGGAG 3120  
QY 3121 GGAAGAGAGAGAGAGAGTGTGAGAACATTCCTGTGATTTCTGCTGAGGAG 3180  
Db 3121 GGAAGAGAGAGAGAGAGTGTGAGAACATTCCTGTGATTTCTGCTGAGGAG 3180  
QY 3181 CAGAGAGAGAGAGAGTGTGAGAACATTCCTGTGATTTCTGCTGAGGAG 3240  
Db 3181 CAGAGAGAGAGAGAGTGTGAGAACATTCCTGTGATTTCTGCTGAGGAG 3240  
QY 3241 TCCCTAAGCATAGACATGCAATTTGCAATTAACCAAAAGAAATGAGAGTACTGAGT 3300  
Db 3241 TCCCTAAGCATAGACATGCAATTTGCAATTAACCAAAAGAAATGAGAGTACTGAGT 3300

QY 3301 GGTAGCTTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360  
Db 3301 GGTAGCTTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360  
QY 3361 TTAAATCTTTCACCTGAGCAGAGACCCAGAGAGTCAAGTCAAGTCAAGTCAAG 3420  
Db 3361 TTAAATCTTTCACCTGAGCAGAGACCCAGAGAGTCAAGTCAAGTCAAGTCAAG 3420  
QY 3421 AGTGAAGTCAAG 3480  
Db 3421 AGTGAAGTCAAG 3480  
QY 3481 ACAGATTCATTAAG 3540  
Db 3481 ACAGATTCATTAAG 3540  
QY 3541 GTTCTAG 3600  
Db 3541 GTTCTAG 3600  
QY 3601 CTTGATTTCTAATTAATTTTCTTCTTCAAGTCAAGTCAAGTCAAGTCAAG 3660  
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QY 3601 CTTGATTTCTAATTAATTTTCTTCTTCAAGTCAAGTCAAGTCAAGTCAAG 3660  
Db 3601 CTTGATTTCTAATTAATTTTCTTCTTCAAGTCAAGTCAAGTCAAGTCAAG 3660  
QY 3661 GTAGTAAGTGAAGGAGTGAATTTAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 3720  
Db 3661 GTAGTAAGTGAAGGAGTGAATTTAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 3720  
QY 3721 GAGATTAAG 3780  
Db 3721 GAGATTAAG 3780  
QY 3721 GAGATTAAG 3780  
Db 3721 GAGATTAAG 3780  
QY 3781 TAAAGCAAAAGAGATTCAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3840  
Db 3781 TAAAGCAAAAGAGATTCAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3840  
QY 3841 CATTTAGAGAGATTTACTATCTGATTCAGAAATGAGATTCAGAAATGAGATTCAG 3900  
Db 3841 CATTTAGAGAGATTTACTATCTGATTCAGAAATGAGATTCAGAAATGAGATTCAG 3900  
QY 3901 TAAACAAACCCAGAGTGTAAATGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3960  
Db 3901 TAAACAAACCCAGAGTGTAAATGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 3960  
QY 3961 AGAATGAATCTTTAG 4020  
Db 3961 AGAATGAATCTTTAG 4020  
QY 4021 AGTTGGAATATTTACTTCAAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 4080  
Db 4021 AGTTGGAATATTTACTTCAAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 4080  
QY 4081 TGCCTAAAG 4140  
Db 4081 TGCCTAAAG 4140  
QY 4141 TTATGAGCTAATTCAGATTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTT 4200  
Db 4141 TTATGAGCTAATTCAGATTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTT 4200  
QY 4201 GGAATTTAATCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 4260  
Db 4201 GGAATTTAATCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 4260  
QY 4261 TGTTTTACAGCTTTCAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 4320  
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QY 4321 CTCAAGTGTAAATTAACAGTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 4380  
Db 4321 CTCAAGTGTAAATTAACAGTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 4380  
QY 4381 TTATATCATATTAACAGTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 4440  
Db 4381 TTATATCATATTAACAGTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 4440

[illegible]

OS	Homo sapiens.
XX	
XX	W09832850-A1.
PD	
XX	30-JUL-1998.
PF	09-JAN-1998; 98WC-US000468.
XX	
XX	28-JAN-1997; 97US-00791154.
PR	26-SEP-1997; 97US-00938669.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PI	Nguyen TD, Polansky JR, Chen P, Chen H;
DR	WPI; 1998-427946/36.
PT	
XX	
PS	Use of TIGR nucleic acid sequences - used for, e.g. developing products for diagnosis, prognosis and treatment of glaucoma.
XX	
XX	Claim 34; Fig 1; 105pp; English.
CC	This sequence is a trabecular meshwork induced glucocorticoid response protein (TIGP) promoter region which is used in a method for diagnosing glaucoma in a patient. The method involves the detection of polymorphisms whose presence is predictive of a mutation affecting TIGR response in the patient and can be diagnostic of glaucoma or steroid sensitivity. Base substitutions and base additions upstream of and within TIGR exons can also be used to diagnose glaucoma
CC	
XX	
SQ	Sequence 5299 BP; 1482 A; 1151 C; 1235 G; 1431 T; 0 U; 0 Other;
Query Match	99.5%; Score 5246.4; DB 2; Length 5299;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 5269; Conservative	0; Mismatches 1; Indels 2; Gaps 2
OY	1 ATCTTTGTCAGTTTAACCTCAGGGCTATTATGAATAAGATACCAGATGTGAAG 60
DB	1 ATCTTTGTCAGTTTAACCTCAGGGCTATTATGAATAAGATACCAGATGTGAAG 60
OY	61 TCCATATAAAGTGATGCCTCATCGGATGATGTCCTTGGCAGATGATTAAGAATCA 120
DB	61 TCCATATAAAGTGATGCTCCATTCGGATGATGTCCTTGGCAGATGATTAAGAATCA 120
OY	121 GGAAGAGAGATATCCAGCTTAGGCCAAGTGTCAAGGCTGTGTCTCTTATTTTAGTA 180
DB	121 GGAAGAGAGATATCCAGCTTAGGCCAAGTGTCAAGGCTGTGTCTCTTATTTTAGTA 180
OY	181 CAATGTGCTCTGACGGAAGCTATTCTTAGAAACATCACATCCAATATGTAAATC 240
DB	181 CAATGTGCTCTGACGGAAGCTATTCTTAGAAACATCACATCCAATATGTAAATC 240
OY	241 CATCAAACGAGACTAAGAAACAGGAATGAGATGGGACCTTGCCCAAGAAAAATCCAG 300
DB	241 CATCAAACGAGACTAAGAAACAGGAATGAGATGGGACCTTGCCCAAGAAAAATCCAG 300
OY	301 GAGAGCAATTAATGATGAAAAATAAATCTTTCCTTGTTTTAAATTCAGAAAAAATG 360
DB	301 GAGAGCAATTAATGATGAAAAATAAATCTTTCCTTGTTTTAAATTCAGAAAAAATG 360
OY	361 ATGAGAGCCAAAATCAATGAATTAAGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATGG 420
DB	361 ATGAGAGCCAAAATCAATGAATTAAGAAAAACAGCTCAGAAAAAAGATGTTTCCAAATGG 420
OY	421 TAATTAAATTTGTTCTCTGGGAAAGAGACCTCATGTGAGCTTGATGGAAAAATGGAA 480
DB	421 TAATTAAATTTGTTCTCTGGGAAAGAGACCTCATGTGAGCTTGATGGAAAAATGGAA 480
OY	481 AAACGTCAAACATGATCTGATCAGATCCCAGAAATGAGATTAATTTTAAAAACAGAT 540
DB	481 AAACGTCAAACATGATCTGATCAGATCCCAGAAATGAGATTAATTTTAAAAACAGAT 540
OY	541 GGATCACTCTGGGAGCAAGTTCAAGAAAGTCAATGTTACAAAGACAATAACATAAC 600

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Db 541 GGCATCACTCTGGGGAGGCAAGTTCAGAAAGTCATGTTAGCAAAAGACATACATTAAC 600
Qy 601 AGCAAAATCAAAATTTCCGCAATATGCAAGAGAAATAGGGACTGGGAAAGCTTTCATAC 660
Db 601 AGCAAAATCAAAATTTCCGCAATATGCAAGAGAAATAGGGACTGGGAAAGCTTTCATAC 660
Qy 661 AGTATTAGGCACTTGAACCATGTTGGCAACCTCCCGCTTATACAGAGAAACAAAA 720
Db 661 AGTATTAGGCACTTGAACCATGTTGGCAACCTCCCGCTTATACAGAGAAACAAAA 720
Qy 721 ATTGACTGGGCTAAGCTTGACTTTCAAGGGAATATGAAAACTAGAGCAAAACAAA 780
Db 721 ATTGACTGGGCTAAGCTTGACTTTCAAGGGAATATGAAAACTAGAGCAAAACAAA 780
Qy 781 GACATGGTTAAAAGGCAACCAACATTTGAGCCTTCAAGCAGCAGTCCCTCAGCA 840
Db 781 GACATGGTTAAAAGGCAACCAACATTTGAGCCTTCAAGCAGCAGTCCCTCAGCA 840
Qy 841 GGGACCCCTGAGGCAATTGGCTTTAGGAAGGCAAGTTTCTTAAAGAACTC 900
Db 841 GGGACCCCTGAGGCAATTGGCTTTAGGAAGGCAAGTTTCTTAAAGAACTC 900
Qy 901 TTGAAGATCATGAATTTTAACATTTTAAGTATTAACAAATATGCGATGATATCAG 960
Db 901 TTGAAGATCATGAATTTTAACATTTTAAGTATTAACAAATATGCGATGATATCAG 960
Qy 961 TTTAGACATGGGTCCCAATTTTATTAAGTCAAGCATACAAAGATTAACGATCCAGCTC 1020
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Qy 1021 GGATAGGTCAGAATCAATTAGAAATCACTGTGCCCATCTAAGCTTTTTCAGAAATGATC 1080
Db 1021 GGATAGGTCAGAATCAATTAGAAATCACTGTGCCCATCTAAGCTTTTTCAGAAATGATC 1080
Qy 1081 TGTCAATAGCCCTCAACACAGAGCCCGATGTGTCTGACCTACACATCTACACCCAA 1140
Db 1081 TGTCAATAGCCCTCAACACAGAGCCCGATGTGTCTGACCTACACATCTACACCCAA 1140
Qy 1141 GTGCTCAACCATGTTAAGGTGATCATCTAGTAGGTCATACAAATGCAACCTCC 1200
Db 1141 GTGCTCAACCATGTTAAGGTGATCATCTAGTAGGTCATACAAATGCAACCTCC 1200
Qy 1201 TGTGACAGCCCATCCCGCTCAACAGAAAGTCTCCCACTCTAGACTCTGATCAGATGT 1260
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Db 1321 ACCGAGCTCACTGCAACCTCTGCTCCAGGTTCAAGCAATCTCTGCTCAGCCTCC 1380
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Qy 1441 GTTTCACCACTATTAAGCCCGGTGTCTTGAACCTCTGACCTCAGAGATCACCACCTC 1500
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Db 1561 TTAATTAAGGAATTACTGAATGTTTCTAAACCAACAGGGAACAGCAAAAGCTGTGA 1620
Qy 1621 TAAATTCAGGATTCCTTGGATGGGAAATGGTGCATGAGCTGCTGCTAGTCCAGAC 1680
Db 1621 TAAATTCAGGATTCCTTGGATGGGAAATGGTGCATGAGCTGCTGCTAGTCCAGAC 1680

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Db 1681 CACTGTGCTCATCACTTTCTTCCTCATCTCATATTTTGAAGCTTAAGTATCAATTTTAT 1740
Qy 1741 CACATGCTTTTGTGTAAGCTCTCCATCTGTTACTGAATATAGATATACATAACTAG 1800
Db 1741 CACATGCTTTTGTGTAAGCTCTCCATCTGTTACTGAATATAGATATACATAACTAG 1800
Qy 1801 TTCCATTTGGGGCACTGTGTGTGTGTATAGAGGAGAGGAGGCTGACAGCCTCCCT 1860
Db 1801 TTCCATTTGGGGCACTGTGTGTGTGTATAGAGGAGAGGAGGCTGACAGCCTCCCT 1860
Qy 1861 TGAAGCCCGGGAGAGGTTTCTCCACAGCTGGGGAGGAGGCTGACAGCCTCCGAGTCC 1920
Db 1861 TGAAGCCCGGGAGAGGTTTCTCCACAGCTGGGGAGGAGGCTGACAGCCTCCGAGTCC 1920
Qy 1921 TGGGTGTCTGAGCAACTGTGCGCAGCCCGTGCACCTGTTGTTTGTATCACTCTAGG 1980
Db 1921 TGGGTGTCTGAGCAACTGTGCGCAGCCCGTGCACCTGTTGTTTGTATCACTCTAGG 1980
Qy 1981 GACCTGTGCTTTCTATTTCTGTGTACTCTCTTCAATCAACAGGATTCATTTGACAT 2040
Db 1981 GACCTGTGCTTTCTATTTCTGTGTACTCTCTTCAATCAACAGGATTCATTTGACAT 2040
Qy 2041 TATTGAGTACTTATCTGACAGACACAGAGCAAAATGTTGAGCAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATCTGACAGACACAGAGCAAAATGTTGAGCAAGCAGTCACTGC 2100
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Db 2341 GCTCGCTTCCCGTGAATGCTCTGTGTGATCTGAGCTGAGACTCTTGGCTCAGGCT 2400
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Db 2401 CCAGAAAGAAATGAGAGAGGAAATGATCTTAAACGAGAAATTCGAGGGGACAGTGTTC 2460
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Db 2521 TGGGAGAGCTGGGGCTGAGCGGAGTGTAAAGGCAAGAGTGA 2580
Qy 2581 GCTGCCAGATGTTGAGTGTGTCAAGGGGCTGGGAGTTTCCGTTGCTCTGTGAGC 2640
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Qy 2641 CTTTATCTTTTCTGCTGAGAGAGAAAGTCTAATTTCAAGAAAGATGACATTC 2700
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Db 2701 ATAAAGTCACTGTAAATTCAGAGGTGTGATGAGTCTTCTTCAAGAAAGCTTTAT 2760

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2761 TTATGGGAATATAGAGACGAGCTCATTTCTAGGCGCTTAATTACAGGAAGAAGTAC 2820  
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Db 3661 GTAGTACTGAG 3720  
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Db 4080 TTGCTCAAGCAATCATATTTTCAAGAGCTTAAATTTCTGACAGTTTGGTATA 4139  
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Db 4200 GGAATTAATTAACCTAG 4259  
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Qy 4560 TAT 4619  
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Db 4920 GTGAATGGAAT 4979



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QY 721 ATTGAATGAGGCTAAGCTGAGCTTTCAGAGGAAATATGAAAACTGAGAGGAAACAAAA 780  
Db 721 ATTGAATGAGGCTAAGCTGAGCTTTCAGAGGAAATATGAAAACTGAGAGGAAACAAAA 780  
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QY 1801 TTCATTTGGGGCCATCTGTGTGTGTATGAGGAGGAGGAGGATACCCAGAGACTCT 1860  
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QY 1861 TGAAGCCCCCGCAGAGGTTTCTCTCCAGCTGGGGAGCTTCGAAACAACCCGAGGCTC 1920  
Db 1861 TGAAGCCCCCGCAGAGGTTTCTCTCCAGCTGGGGAGCTTCGAAACAACCCGAGGCTC 1920  
QY 1921 TGGGTCTGAGGAACCTGCGCAGCCGTCGACCTGTTTGTATATCATCTCTAG 1980  
Db 1921 TGGGTCTGAGGAACCTGCGCAGCCGTCGACCTGTTTGTATATCATCTCTAG 1980  
QY 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTGTCATTCATTCAGGCAATTCATGACAAT 2040  
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTGTCATTCATTCAGGCAATTCATGACAAT 2040  
QY 2041 TATTGAGTACTTATATCTGCCAGCACCAAGACAAATGATGAGCAAGCACTCCTC 2100  
Db 2041 TATTGAGTACTTATATCTGCCAGCACCAAGACAAATGATGAGCAAGCACTCCTC 2100  
QY 2101 CCTACCTTCGTGAGGTGACAGTTTCTCATGAAAGCTGACAGAAATTAATAGCA 2160  
Db 2101 CCTACCTTCGTGAGGTGACAGTTTCTCATGAAAGCTGACAGAAATTAATAGCA 2160  
QY 2161 GCCAATTTAAACCCAGTGTGAAAGAAAGAAATTAACATCTTGAAGATTTGCGC 2220  
Db 2161 GCCAATTTAAACCCAGTGTGAAAGAAAGAAATTAACATCTTGAAGATTTGCGC 2220  
QY 2221 AGCATCCCTTAAAGGCAACCTCCCTAGGCGCCGCTGCTCATGCTGCTGCGCGAG 2280  
Db 2221 AGCATCCCTTAAAGGCAACCTCCCTAGGCGCCGCTGCTCATGCTGCTGCGCGAG 2280  
QY 2281 CCCCCAGCCGAGTCTTCAAGCTCTCTCTCATGATGATCAAGGCTGCACTGCT 2340  
Db 2281 CCCCCAGCCGAGTCTTCAAGCTCTCTCTCATGATGATCAAGGCTGCACTGCT 2340  
QY 2341 GCTGCTCCCGGAGATGCTGCTGAGTGCATGAGTGAAGCTGCTGCTGCTGCTGCT 2400  
Db 2341 GCTGCTCCCGGAGATGCTGCTGAGTGCATGAGTGAAGCTGCTGCTGCTGCTGCT 2400  
QY 2401 CCAAGAAAGAAATGAGAGGAGAACTAGCTTAACGAGAACTGAGAGGAGCAGTGTTC 2460  
Db 2401 CCAAGAAAGAAATGAGAGGAGAACTAGCTTAACGAGAACTGAGAGGAGCAGTGTTC 2460  
QY 2461 CTGAGAGGAAAGGAGGCTCCAGCTCCAGGAAATTCAGAGAGTGGGACTGCAAGGAG 2520  
Db 2461 CTGAGAGGAAAGGAGGCTCCAGCTCCAGGAAATTCAGAGAGTGGGACTGCAAGGAG 2520  
QY 2521 TGGGAGCGCTGGGCTGAGCGGCTGCTGAAGGCAAGGAGGAAAGGCAAGGCTGTA 2580  
Db 2521 TGGGAGCGCTGGGCTGAGCGGCTGCTGAAGGCAAGGAGGAAAGGCAAGGCTGTA 2580  
QY 2581 GCTGCCAGATGTTCACTGTGTTTACAGGGGCTGGGAGTTTCTGCTGCTGCTGAGC 2640  
Db 2581 GCTGCCAGATGTTCACTGTGTTTACAGGGGCTGGGAGTTTCTGCTGCTGCTGAGC 2640  
QY 2641 CTTTATCTTTTCTGCTGCTGAGGAGAAAGTCTATTTCTAGAGGAGATGCACTTC 2700  
Db 2641 CTTTATCTTTTCTGCTGCTGAGGAGAAAGTCTATTTCTAGAGGAGATGCACTTC 2700  
QY 2701 AATAAGTCACTGTTAAATTCAGAGGTGTCATGAGGTTTCTTCAAGAGCCCTTAT 2760  
Db 2701 AATAAGTCACTGTTAAATTCAGAGGTGTCATGAGGTTTCTTCAAGAGCCCTTAT 2760  
QY 2761 TTAATGGGAATTAAGAGAGGAGCTCATTTCCAGGCGCTTAATTCAGAGAGAGTGC 2820  
Db 2761 TTAATGGGAATTAAGAGAGGAGCTCATTTCCAGGCGCTTAATTCAGAGAGAGTGC 2820

QY 2821 TGGAGCTTTTCTTTCATGTCTTCTGGGCACTACTCAGCCCTGTGTGACTTGGCTTA 2880  
Db 2821 TGGAGCTTTTCTTTCATGTCTTCTGGGCACTACTCAGCCCTGTGTGACTTGGCTTA 2880  
QY 2881 TCGAAGACGGTGGAAAACCTTGGATCAGAGAACCGGTTTTCTTCTGGTCCGCAAT 2940  
Db 2881 TCGAAGACGGTGGAAAACCTTGGATCAGAGAACCGGTTTTCTTCTGGTCCGCAAT 2940  
QY 2941 GGTGGCTGTGCAACCGTGGGCAAGTGTCTCTCCCTGGGCCATAGTCTTCTGCT 3000  
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QY 3061 GATGTGAGAGGGGGAAGAGGAGAGCTGAGAGCTGAGAGCCAGGGGAGTGAAGG 3120  
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QY 3121 GGAAGAGAGGAGGAGAGAGCTGGGTGCTCCATGATGCTGATCAGTCACTC 3180  
Db 3121 GGAAGAGAGGAGGAGAGAGCTGGGTGCTCCATGATGCTGATCAGTCACTC 3180  
QY 3181 CAGGACCGAGAGCCATAGCTTCCAGGAAAGCTCAATGAACCCAGGCACTTTTCT 3240  
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QY 3301 GGTAGCTTTTCTGCTGCTCAAAAACCTGGGCCAGAGCAAGTGAAGAAATGCCAGATT 3360  
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QY 3421 AGTAGCTGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480  
Db 3421 AGTAGCTGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480  
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Db 3481 ACAGATTCATTTCAAGGGCAGTGAAGATGACAGAGAGATTAATGTCACGATCTGG 3540  
QY 3541 GTTCTAGAGAGGAGGCTATATTGTGGGGGGAATAATCAGTTCAAGGAGTCCGAGA 3600  
Db 3541 GTTCTAGAGAGGAGGCTATATTGTGGGGGGAATAATCAGTTCAAGGAGTCCGAGA 3600  
QY 3601 CCTGATTTCTAATATCTATATTTTCTTTAAGAGCTGAGTATTTGACCAAGTCAAG 3660  
Db 3601 CCTGATTTCTAATATCTATATTTTCTTTAAGAGCTGAGTATTTGACCAAGTCAAG 3660  
QY 3661 GTACTAAGTGAAGTGAAGATTAAGTTCCTTTAGGAACTTTTCTCTGT 3720  
Db 3661 GTACTAAGTGAAGTGAAGATTAAGTTCCTTTAGGAACTTTTCTCTGT 3720  
QY 3721 GGAATAGCAGCAGAGGAGATCCGTTCTTTTAAAGAGAAACATTTCTTAAGG 3780  
Db 3721 GGAATAGCAGCAGAGGAGATCCGTTCTTTTAAAGAGAAACATTTCTTAAGG 3780  
QY 3781 TAAAGCCAAAGATTTAAGCTTGTGCTGCTGATATATGTTTTTTTGAAGAAAT 3840  
Db 3781 TAAAGCCAAAGATTTAAGCTTGTGCTGCTGATATATGTTTTTTTGAAGAAAT 3840  
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Db 3841 CATTTAGAGGATGTTTACTATCTGATTCAGAAATGAGACTAGTACCTTTGGTCACTG 3900

QY 3901 TAAAGAAACCCAGTGTAAATGTCACAAAGTTCAGGCTTACTGCAAGAACCAATCAA- 3959  
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QY 3960 AAGATAGATCTTTAGAGCAACCTGTTTTCTCCATCTGAGAGTGTGCTCCAGG 4019  
Db 3960 AAGATAGATCTTTAGAGCAACCTGTTTTCTCCATCTGAGAGTGTGCTCCAGG 4019  
QY 4020 CAGTTGGAATATTTAATTGACAAAGTATGACCTGTGTGGAATTAACAATAAG 4079  
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QY 4080 TTGCTCAAGGCAATCAATTTCAAGGCTTAAAGTACTTGAAGTGTGATATA 4139  
Db 4080 TTGCTCAAGGCAATCAATTTCAAGGCTTAAAGTACTTGAAGTGTGATATA 4139  
QY 4140 TTTATGCTATTCAGATTTGCTTTTGTCTTTGCTTTGATTAATGTAAGCA 4199  
Db 4140 TTTATGCTATTCAGATTTGCTTTTGTCTTTGCTTTGATTAATGTAAGCA 4199  
QY 4200 GGGATTAATTAACCTACAGTCCAGAAAGCTGGAATTTGAATGAGAAAAATTAACAT 4259  
Db 4200 GGGATTAATTAACCTACAGTCCAGAAAGCTGGAATTTGAATGAGAAAAATTAACAT 4259  
QY 4260 TTTGTTTTTCAACCTTCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4319  
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QY 4499 ACTTGAATTAAGACCTCTGCTGATCTGATTTTAAATTAATTAATTAATTAATTAAT 4559  
Db 4499 ACTTGAATTAAGACCTCTGCTGATCTGATTTTAAATTAATTAATTAATTAATTAAT 4559  
QY 4500 AATTTGAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4559  
Db 4500 AATTTGAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4559  
QY 4560 TATATATTTGAAAAATCTTTCTGAGAGAGTCCCAAGATTTCAACCAATGAGTTCTG 4619  
Db 4560 TATATATTTGAAAAATCTTTCTGAGAGAGTCCCAAGATTTCAACCAATGAGTTCTG 4619  
QY 4620 GCATGACACACACAGATTAAGATTTTGAAGGCTTAATGAATTTGATTTGATTTG 4679  
Db 4620 GCATGACACACACAGATTAAGATTTTGAAGGCTTAATGAATTTGATTTGATTTG 4679  
QY 4680 ATGCAAGACGAAATTAAGAAAGTTCACCAAGATTAACAGTGTGTTTAAAGTAAAGG 4739  
Db 4680 ATGCAAGACGAAATTAAGAAAGTTCACCAAGATTAACAGTGTGTTTAAAGTAAAGG 4739  
QY 4740 GAGGGGGAATATGCGCTTCTTAAGAGATGCTTCTGAGAGCTGATGAGGCTGCT 4799  
Db 4740 GAGGGGGAATATGCGCTTCTTAAGAGATGCTTCTGAGAGCTGATGAGGCTGCT 4799  
QY 4800 CTTTGTCTGCTGCTGCTGCTTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859  
Db 4800 CTTTGTCTGCTGCTGCTGCTTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859  
QY 4860 TGAATCTCAGTTCTAAGATAGTGCCTGAGCAGTGAAGGTTTCAATGAGTTGACAG 4919  
Db 4860 TGAATCTCAGTTCTAAGATAGTGCCTGAGCAGTGAAGGTTTCAATGAGTTGACAG 4919  
QY 4920 GTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4979  
Db 4920 GTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4979  
QY 4980 GTGTAGTGTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5039



Accession	Sequence	Length
Dh	GTCTAGTGTGTGTCAGTGTGTGTGTGTGTGTGTGTGTGTGTAAACAGGTGAGT	5039
Qy	ATAGGACATATATGTGGGTATGGGTGCATPAAATGGGAGTCTTTTAAACAACT	5099
Dh	ATRGACATTTATTTGGGTATGGGTGCATPAAATGGGAGTCTTTTAAACAACT	5099
Qy	CCAAACAGCTTCTGGAGTTATTTTCTAAGAACTTCTGTGGCAGCTGAAGCAACC	5159
Dh	CCAAACAGCTTCTGGAGTTATTTTCTAAGAACTTCTGTGGCAGCTGAAGCAACC	5159
Qy	CCCTGTGCACAGCCCCACCCAGCTCTACGTGGCACCTCTGTCTTCCCATGAAGGCT	5219
Dh	CCCTGTGCACAGCCCCACCCAGCTCTACGTGGCACCTCTGTCTTCCCATGAAGGCT	5219
Qy	GGCTCCCGCATATATTAACCTCTCTGGAGCTCGGCGATGAGCCAGCAAG	5271
Dh	GGCTCCCGCATATATTAACCTCTCTGGAGCTCGGCGATGAGCCAGCAAG	5271

## RESULT 6

ID	AAV51365 standard; DNA; 5300 BP.
XX	
AC	AAV51365;
DT	27-OCT-1998 (first entry)
XX	
DE	Human TIGR promoter mutant TIGRmt4 DNA.
XX	
KM	TIGR; trabecular meshwork induced glucocorticoid response protein; human; diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX	
OS	Homo sapiens.
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	4256
FT	/*tag= a
FT	/note= "Wild-type A is replaced by G"
XX	
PN	MO9812850-A1.
XX	
PD	30-JUL-1998.
XX	
PF	09-JAN-1998; 98WO-US000468.
XX	
PR	28-JAN-1997; 97US-00791154.
PR	26-SEP-1997; 97US-00938669.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PI	Nguyen TD, Polansky JR, Chen P, Chen H;
XX	
DR	WPI; 1998-427946/36.
XX	
PT	Use of TIGR nucleic acid sequences - used for, e.g. developing products for diagnosis, prognosis and treatment of glaucoma.
XX	
PS	Disclosure; Fig 2; 105bp; English.
XX	
CC	This sequence is a trabecular meshwork induced glucocorticoid response protein (TIGR) promoter mutant, TIGRmt4, which is used in a method for diagnosing glaucoma in a patient. The method involves the detection of polymorphisms whose presence is predictive of a mutation affecting TIGR response in the patient and can be diagnostic of glaucoma or steroid sensitivity. Base substitutions and base additions upstream of and within TIGR exons can also be used to diagnose glaucoma
XX	
CC	Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 U; 0 Other;
XX	

Sequence	5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 U; 0 Other;
Query Match	99.5%; Score 5244.8; DB 2; Length 5300;
Best Local Similarity	99.9%; Pred. No. 0;

	Matches	5288; Conservative	0; Mismatches	2; Indels	2; Gaps	2						
QY	1	ATCTTTGTTCA	GATTTA	CTTCAG	GCGTAT	TTATGA	ATAATG	AAGATAC	CAATGTG	AAAG	60	
Db	1	ATCTTTGTTCA	GATTTA	CTTCAG	GCGTAT	TTATGA	ATAATG	AAGATAC	CAATGTG	AAAG	60	
QY	61	TCCATATTA	CTGATAG	CCCTCATT	CGAGTGA	TGATGCTTTT	GGCAG	AGATGA	TAAGA	ATA	120	
Db	61	TCCATATTA	CTGATAG	CCCTCATT	CGAGTGA	TGATGCTTTT	GGCAG	AGATGA	TAAGA	ATA	120	
QY	121	GGAAAGAG	AGTATC	CACTAG	CCAGTA	GTGCAAG	GCTGTGTCTG	CTTATTTA	TGTA		180	
Db	121	GGAAAGAG	AGTATC	CACTAG	CCAGTA	GTGCAAG	GCTGTGTCTG	CTTATTTA	TGTA		180	
QY	181	CAGATGTG	CTCTG	CAGAA	AGCTAT	TTCTTAG	AGAAACAT	CAATCC	AATATG	ATAATC	240	
Db	181	CAGATGTG	CTCTG	CAGAA	AGCTAT	TTCTTAG	AGAAACAT	CAATCC	AATATG	ATAATC	240	
QY	241	CATCAAA	CAGAG	ACTAG	AAACAG	GAATG	AGATGG	CACTTG	CCCAAG	AAAAATG	300	
Db	241	CATCAAA	CAGAG	ACTAG	AAACAG	GAATG	AGATGG	CACTTG	CCCAAG	AAAAATG	300	
QY	301	GAGAG	CAATTA	TGATGA	AAAAATAA	CTTTTCC	CTTTGTTT	TAATTC	AGAAAAATG		360	
Db	301	GAGAG	CAATTA	TGATGA	AAAAATAA	CTTTTCC	CTTTGTTT	TAATTC	AGAAAAATG		360	
QY	361	ATGAG	AGCCAA	AATCA	TGATGA	AAAAA	CAGCTC	AGAAAA	AAAGATG	TTCCAAATGG	420	
Db	361	ATGAG	AGCCAA	AATCA	TGATGA	AAAAA	CAGCTC	AGAAAA	AAAGATG	TTCCAAATGG	420	
QY	421	TAATTA	AGTATTT	GTTCCT	TGG	AAGAG	ACCTCC	ATGATG	ACTGAT	TGGAAAAATGG	480	
Db	421	TAATTA	AGTATTT	GTTCCT	TGG	AAGAG	ACCTCC	ATGATG	ACTGAT	TGGAAAAATGG	480	
QY	481	AAACG	CAAA	AAACA	AGATCT	GTATCA	ATCC	CAAGTGG	ATATATTT	TAATAAAC	540	
Db	481	AAACG	CAAA	AAACA	AGATCT	GTATCA	ATCC	CAAGTGG	ATATATTT	TAATAAAC	540	
QY	541	GGCAT	CACTCT	GGGAG	GCAAGTTC	CAGAA	AGTATG	TAGCA	AAAGACAT	ATAACATAC	600	
Db	541	GGCAT	CACTCT	GGGAG	GCAAGTTC	CAGAA	AGTATG	TAGCA	AAAGACAT	ATAACATAC	600	
QY	601	AGCAAA	TAAT	TAATA	TTCCG	CAATG	CAG	AGAAAA	TCGGAA	AGCTTT	TAATAC	660
Db	601	AGCAAA	TAAT	TAATA	TTCCG	CAATG	CAG	AGAAAA	TCGGAA	AGCTTT	TAATAC	660
QY	661	AGGAT	ATTAG	GCA	AGTTGA	CAATGTT	TGGA	CAACCT	CCCGCT	ATAC	720	
Db	661	AGGAT	ATTAG	GCA	AGTTGA	CAATGTT	TGGA	CAACCT	CCCGCT	ATAC	720	
QY	721	ATTGAT	CTGG	CTA	AGCTG	GA	CTTTCA	AGG	AAATATG	AAAAATG	780	
Db	721	ATTGAT	CTGG	CTA	AGCTG	GA	CTTTCA	AGG	AAATATG	AAAAATG	780	
QY	781	GACAT	GGTTAA	AAAG	CAAC	CAGAA	CA	TTG	GA	CGCTTCA	AAAGAG	840
Db	781	GACAT	GGTTAA	AAAG	CAAC	CAGAA	CA	TTG	GA	CGCTTCA	AAAGAG	840
QY	841	GGGAC	CCCTG	AGG	CA	TTTG	CCCTT	TGA	AGG	CCAGTTT	CTTAA	900
Db	841	GGGAC	CCCTG	AGG	CA	TTTG	CCCTT	TGA	AGG	CCAGTTT	CTTAA	900
QY	901	TTGAA	AGAT	CA	TGA	ATTTTAA	CCATTT	TAA	GTAT	AAACAA	TATG	960
Db	901	TTGAA	AGAT	CA	TGA	ATTTTAA	CCATTT	TAA	GTAT	AAACAA	TATG	960
QY	961	TTTAA	GCAT	GGGTCC	CAATTT	TAT	AAAGT	CA	AGCA	TAC	AGATAC	1020
Db	961	TTTAA	GCAT	GGGTCC	CAATTT	TAT	AAAGT	CA	AGCA	TAC	AGATAC	1020
QY	1021	GGAT	AGT	GC	AG	AAAT	CA	TAT	GA	AAAT	CA	1080
Db	1021	GGAT	AGT	GC	AG	AAAT	CA	TAT	GA	AAAT	CA	1080

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QY 1081 TGTGATAGCCCTGACACACAGGCGCGATGTGTCTGATCCTACACACATCTTACACCCAA 1140
Db 1081 TGTGATAGCCCTGACACACAGGCGCGATGTGTCTGATCCTACACACATCTTACACCCAA 1140
QY 1141 GTGGCCCTCAACCAATGTTGATGCTGTCACTCACTAGTATGCTCCATTTACAAATGCGACCTCCC 1200
Db 1141 GTGGCCCTCAACCAATGTTGATGCTGTCACTCACTAGTATGCTCCATTTACAAATGCGACCTCCC 1200
QY 1201 TGTGACAGCCATCCGCTCCACAGAGAGTCTCCCACTCTAGACTTCTGCAATCAGATGT 1260
Db 1201 TGTGACAGCCATCCGCTCCACAGAGAGTCTCCCACTCTAGACTTCTGCAATCAGATGT 1260
QY 1261 TACAGCCAGAGTCCGTGAGGGTGAAGGCTGTGTCTTACACCTAGCTGATGTCTAC 1320
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QY 1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGGTTCCAGCAATTCCTGTCTGACCTCC 1380
Db 1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGGTTCCAGCAATTCCTGTCTGACCTCC 1380
QY 1381 CGGTAGCTGGAGCTACAGCGGACCGCGCTAATTTTGTATGTTAGTATGAGATGG 1440
Db 1381 CGGTAGCTGGAGCTACAGCGGACCGCGCTAATTTTGTATGTTAGTATGAGATGG 1440
QY 1441 GTTTCACATATAGCCCGCTGTCTTGAATCTCGACTGAGTGAATCCACCCACTC 1500
Db 1441 GTTTCACATATAGCCCGCTGTCTTGAATCTCGACTGAGTGAATCCACCCACTC 1500
QY 1501 AGCTCTCTAAAGTCTGGGATTAACAGGATGAGTCAACGCGCGCCGCAAGGCTAGT 1560
Db 1501 AGCTCTCTAAAGTCTGGGATTAACAGGATGAGTCAACGCGCGCCGCAAGGCTAGT 1560
QY 1561 TTAATAAGGAATTAAGTATGATGTTACTAATAACCAACAGAGAAACAGCAAAAGTGTGA 1620
Db 1561 TTAATAAGGAATTAAGTATGATGTTACTAATAACCAACAGAGAAACAGCAAAAGTGTGA 1620
QY 1621 TAAATTCAGGGAATCTTGGGATGGGAAATGTGTCATGAGTCTGCTGCTAGTCCCAAC 1680
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Db 1681 CACTGCTCTCATCATCTTCTTCCCTCATCCCTCATTTTCAAGGTAAGTATACATTTAAT 1740
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Db 1741 CACCATGCTTTTGTGTAAGCTCCACATGTTACTGAAATAGAGTATACATAAATAG 1800
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QY 1861 TGAAGCCCCCGGAGAGGTTTCTCTCAGCTGGGAGAGGCTGCAAGCAACCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGAGAGGTTTCTCTCAGCTGGGAGAGGCTGCAAGCAACCGGGGTCC 1920
QY 1921 TGGGTGTCTGAGCAACCTGCAAGCCGCTGCACTGCTGTGTGTGTATCACTCTCTAG 1980
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QY 1981 GACCTGTGCTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
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QY 2101 CCTACCTTGTGTAGGAGTCAAGTTCTCATGGAAGGTGCAAGAAATTAATGACA 2160
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QY 2401 CCAAGAAAGAAATGAGAGAGGAAACTAGTCTTAAAGGAAATCTGAGAGGAGCAGTGTTC 2460
Db 2401 CCAAGAAAGAAATGAGAGAGGAAACTAGTCTTAAAGGAAATCTGAGAGGAGCAGTGTTC 2460
QY 2461 CTCAGAGGAAAGGAGGCTCCACGCTCAGAGAAATTCAGAGAGTGGGAGTGCAGGAG 2520
Db 2461 CTCAGAGGAAAGGAGGCTCCACGCTCAGAGAAATTCAGAGAGTGGGAGTGCAGGAG 2520
QY 2521 TGGGAGCGCTGGGAGCTGAGCGGCTGTGAAAGGCAAGGTGAAGGAGGAGCTGAA 2580
Db 2521 TGGGAGCGCTGGGAGCTGAGCGGCTGTGAAAGGCAAGGTGAAGGAGGAGCTGAA 2580
QY 2581 GCTGCCAGATGTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
Db 2581 GCTGCCAGATGTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
QY 2641 GTTTTATCTTCTCTCTCTGAGAGAGAGATCTATTTATGATGATGAGGATGCACTTC 2700
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QY 2881 TGAAGTCTTTCTTCTTATGCTCTTGTGGGAACTATCTGAGCCCTGTGTGTGTGTGT 2940
Db 2881 TGAAGTCTTTCTTCTTATGCTCTTGTGGGAACTATCTGAGCCCTGTGTGTGTGTGT 2940
QY 2941 GGTGTGTGTGAGACCTGTGGGCAAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3000
Db 2941 GGTGTGTGTGAGACCTGTGGGCAAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3000
QY 3001 ATAAAGACCTTTCAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
Db 3001 ATAAAGACCTTTCAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
QY 3061 GATGTGTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
Db 3061 GATGTGTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
QY 3121 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3180
Db 3121 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3180
QY 3181 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240
Db 3181 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240
QY 3241 TCCTTAAGCATAGACATGAGATTTCGCAATTAACAAAGAAATGAGAGAGTAACTGT 3300
```

Db 3241 TCCCTAGACATAGACATGCAATTTGCCATATACCAAAAAGATGACAGACTAACTGGT 3300  
QY 3301 GGTAGCTTTTGGCTGGCATTTCAAAAACCTGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360  
Db 3301 GGTAGCTTTTGGCTGGCATTTCAAAAACCTGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360  
QY 3361 TTTAACTTTTCAACCTGACACAGCCCAAGCTGACAGTGAATCTGACAGCAAG 3420  
Db 3361 TTTAACTTTTCAACCTGACACAGCCCAAGCTGACAGTGAATCTGACAGCAAG 3420  
QY 3421 AGTACCTGACAGGCAAGGAGAGAGAGAGAGAGAGATAGTGTATGACAGAGAG 3480  
Db 3421 AGTACCTGACAGGCAAGGAGAGAGAGAGAGAGATAGTGTATGACAGAGAG 3480  
QY 3481 ACAGATTCATTCAGAGGCAAGTGGAAATGACACAGGATTAATGTCACAGTATCTGG 3540  
Db 3481 ACAGATTCATTCAGAGGCAAGTGGAAATGACACAGGATTAATGTCACAGTATCTGG 3540  
QY 3541 GTTCTAGAGGCAAGGCTATTTGTGGGGGAAAAAATCAGTTCAAGGAAATGCGGAGA 3600  
Db 3541 GTTCTAGAGGCAAGGCTATTTGTGGGGGAAAAAATCAGTTCAAGGAAATGCGGAGA 3600  
QY 3601 CCTGATTTCTAAATACATATTTTCTTTTCAAGCTGATTAATCTGAGCAAGTCAAG 3660  
Db 3601 CCTGATTTCTAAATACATATTTTCTTTTCAAGCTGATTAATCTGAGCAAGTCAAG 3660  
QY 3661 GTAGTACTAGGCTGTAAAGTACTTATGATTCTCTTATTAGAACTCTTTTCTGT 3720  
Db 3661 GTAGTACTAGGCTGTAAAGTACTTATGATTCTCTTATTAGAACTCTTTTCTGT 3720  
QY 3721 GGAGTTAGAGCAAGGCAATCCCGTTCTTTTAAAGAGAAAGAAACATCTTAAGAG 3780  
Db 3721 GGAGTTAGAGCAAGGCAATCCCGTTCTTTTAAAGAGAAAGAAACATCTTAAGAG 3780  
QY 3781 TAAAGCAAAAGATTCAGCTAGCTGCTGCTGCTATATGATGTTTGTGAAAAAT 3840  
Db 3781 TAAAGCAAAAGATTCAGCTAGCTGCTGCTGCTATATGATGTTTGTGAAAAAT 3840  
QY 3841 CATTTACAGGATGTTTACTATCTGATTAAGAAATAGACATGATCCCTTTGGTCACTG 3900  
Db 3841 CATTTACAGGATGTTTACTATCTGATTAAGAAATAGACATGATCCCTTTGGTCACTG 3900  
QY 3901 TAAACAAACACCCAGTTTAAATGTCAGATTCAGGCTTAATGAGCAAGCAATCAA- 3959  
Db 3901 TAAACAAACACCCAGTTTAAATGTCAGATTCAGGCTTAATGAGCAAGCAATCAA- 3959  
QY 3961 AAGATTAAGATTTTAAAGCAAACTGTGTTCTCAACTGAGAGTGGCAAGG 4019  
Db 3961 AAGATTAAGATTTTAAAGCAAACTGTGTTCTCAACTGAGAGTGGCAAGG 4019  
QY 4020 CAGTTGGAATATTTACTTCAAGATTAAGCACTGTGTTGATTAACAATTAAG 4079  
Db 4020 CAGTTGGAATATTTACTTCAAGATTAAGCACTGTGTTGATTAACAATTAAG 4079  
QY 4080 TTGCTCAAGGCAATCATTTTCAAGTGGCTTAAGTCACTTCAAGTGGTATTA 4139  
Db 4080 TTGCTCAAGGCAATCATTTTCAAGTGGCTTAAGTCACTTCAAGTGGTATTA 4139  
QY 4140 TTTATGCGATGTCATTTGCTTTTCTTTTCTTTGCGTTATTAAGCA 4199  
Db 4140 TTTATGCGATGTCATTTGCTTTTCTTTTCTTTGCGTTATTAAGCA 4199  
QY 4200 GGGATTAATTAACATGACAGTCAAGGCTGATTTGAATGAGAGAAAAATTAACATT 4259  
Db 4200 GGGATTAATTAACATGACAGTCAAGGCTGATTTGAATGAGAGAAAAATTAACATT 4259  
QY 4260 TTGTTTAAACACCTTCTAACTAAATTTACATTTTATTCATTTGCAATAGACCATAA 4319  
Db 4260 TTGTTTAAACACCTTCTAACTAAATTTACATTTTATTCATTTGCAATAGACCATAA 4319  
QY 4320 ACTCAAGTGTAAATTAACAGTACCTGATTTGTCTTAACAATGAATCAAGACAT 4379  
Db 4320 ACTCAAGTGTAAATTAACAGTACCTGATTTGTCTTAACAATGAATCAAGACAT 4379

Db 4320 ACTCAAGTGTAAATTAACAGTACCTGATTTGTCTTAACAATGAATCAAGACAT 4379  
QY 4380 TTTATACATATTAACAGTGTGTCAGATAGCTTTGAAGTGAATATTTATACCAAACT 4439  
Db 4380 TTTATACATATTAACAGTGTGTCAGATAGCTTTGAAGTGAATATTTATACCAAACT 4439  
QY 4440 ACTTGAATTAAGACCTTCTGATGATCTGTTTAACTAATTAATAAACAATGTTAA 4499  
Db 4440 ACTTGAATTAAGACCTTCTGATGATCTGTTTAACTAATTAATAAACAATGTTAA 4499  
QY 4500 AATTTGATATTTGATTAATATATTTCAATATATTTGTTTCTTTGATATATTT 4559  
Db 4500 AATTTGATATTTGATTAATATATTTCAATATATTTGTTTCTTTGATATATTT 4559  
QY 4560 TATATATTTGAAAAATCTTTCTGAGAGAGTTCCCAAGTACAGTGTGTTTAAAGCTAGGGGT 4619  
Db 4560 TATATATTTGAAAAATCTTTCTGAGAGAGTTCCCAAGTACAGTGTGTTTAAAGCTAGGGGT 4619  
QY 4620 GCATGCAACACAGAGTAAAGAACTGATTTAGAGCTTAACATTGACATTGTCCTGAG 4679  
Db 4620 GCATGCAACACAGAGTAAAGAACTGATTTAGAGCTTAACATTGACATTGTCCTGAG 4679  
QY 4680 ATGCAAGCTGAAATTTGAAAGTTCTCCAAAGTACAGTGTGTTTAAAGCTAGGGGT 4739  
Db 4680 ATGCAAGCTGAAATTTGAAAGTTCTCCAAAGTACAGTGTGTTTAAAGCTAGGGGT 4739  
QY 4740 GAGGGGGGAAATCTGCGCTTTCTATAGAAATGCTCTCTGAGAGCTGTAGGGTCTGT 4799  
Db 4740 GAGGGGGGAAATCTGCGCTTTCTATAGAAATGCTCTCTGAGAGCTGTAGGGTCTGT 4799  
QY 4800 CCTGTGTTCTGGCTGCTGTTATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859  
Db 4800 CCTGTGTTCTGGCTGCTGTTATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859  
QY 4860 TGGATCTTCAGATTCCTAGCATAGTGTGCTGAGCAGTGAAGTCTCAATGATGTTGACA 4919  
Db 4860 TGGATCTTCAGATTCCTAGCATAGTGTGCTGAGCAGTGAAGTCTCAATGATGTTGACA 4919  
QY 4920 GTGATGGAATTAATACTGAATATATCTTTGTTGAATGACACACAGTATGCTG 4979  
Db 4920 GTGATGGAATTAATACTGAATATATCTTTGTTGAATGACACACAGTATGCTG 4979  
QY 4980 GTGTAGGTGTGATGCTGT 5039  
Db 4980 GTGTAGGTGTGATGCTGT 5039  
QY 5040 ATAGAACTATTTATGAGGATATGAGTGCATTAATTTGGATGTTCTTTTAAAAAGAACT 5099  
Db 5040 ATAGAACTATTTATGAGGATATGAGTGCATTAATTTGGATGTTCTTTTAAAAAGAACT 5099  
QY 5100 CCAACAGACTTCTGGAAGGTTATTTCTTAAGAACTCTGCTGAGCGTGAAGGCAACC 5159  
Db 5100 CCAACAGACTTCTGGAAGGTTATTTCTTAAGAACTCTGCTGAGCGTGAAGGCAACC 5159  
QY 5160 CCTGTGCAAGCCCAAGGCTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 5219  
Db 5160 CCTGTGCAAGCCCAAGGCTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 5219  
QY 5220 GGTCTCCAGTATTAATAAATCTCTCTGAGCTGCGGCAATGAGCAAGG 5271  
Db 5220 GGTCTCCAGTATTAATAAATCTCTCTGAGCTGCGGCAATGAGCAAGG 5271  
RESULT 7  
AAVS1367  
ID AAVS1367 standard; DNA; 5300 BP.  
XX AAVS1367;  
AC AAVS1367;  
AC AAVS1367;  
DT 27-Oct-1998 (first entry)  
XX Human TIGR promoter variant TIGRsv1 DNA.  
XX



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Db 1501 AGCCTCTAAAGTGTGGGATTTACAGGCATGAGTCAACCGCCGCCGCAAGGCTCAGTGT 1560
Qy 1561 TTAATAAGGAATACTTGAATGATGTTACTAAACCAAGGGAACAGACAAAGCTGTGA 1620
Db 1561 TTATATAGGAATACCTTGAATGATGTTACTAAACCAAGGGAACAGACAAAGCTGTGA 1620
Qy 1621 TAAATTCAGGGAATCTTGGGATGGGGAATGTGCCATGAGCTGTGCTGATGCCAGAC 1660
Db 1621 TAAATTCAGGGAATCTTGGGATGGGGAATGTGCCATGAGCTGTGCTGATGCCAGAC 1660
Qy 1681 CACTGTCCTCATCATCTTCTCCCTCATCTCATTTTCAGGCTAAGTTACATTTAT 1740
Db 1681 CACTGTCCTCATCATCTTCTCCCTCATCTCATTTTCAGGCTAAGTTACATTTAT 1740
Qy 1741 CACCATGCTTTTGTGTGAAGCTTCCACATGCTTACTGAATAAGATATACATAACTAG 1800
Db 1741 CACCATGCTTTTGTGTGAAGCTTCCACATGCTTACTGAATAAGATATACATAACTAG 1800
Qy 1801 TTCCATTTGGGGGCACTGTGTGTGTGTATAGGGGAGAGGCAATCCCGAAGACTTCT 1860
Db 1801 TTCCATTTGGGGGCACTGTGTGTGTGTATAGGGGAGAGGCAATCCCGAAGACTTCT 1860
Qy 1861 TGAAGCCCCCGAGAGAGTTTCTCTCCAGCTGGGGGAGCCCTGGAAGCACCCGGGTC 1920
Db 1861 TGAAGCCCCCGAGAGAGTTTCTCTCCAGCTGGGGGAGCCCTGGAAGCACCCGGGTC 1920
Qy 1921 TGGGTCTCTTGAGCAACCTGCCAGCCGCTGCACTGTGTGTGTGTATCACTCTTAA 1980
Db 1921 TGGGTCTCTTGAGCAACCTGCCAGCCGCTGCACTGTGTGTGTGTATCACTCTTAA 1980
Qy 1981 GACCTGCTCTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
Db 1981 GACCTGCTCTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
Qy 2041 TATGTAGTACTTATTTCTGCCAGACACACAGACAAATGTGTGACAAAGACTGTGC 2100
Db 2041 TATGTAGTACTTATTTCTGCCAGACACACAGACAAATGTGTGACAAAGACTGTGC 2100
Qy 2101 CCTACCTTGTGGAGGTGACAGTTTCTCATGTAAGAGCTGCAGAAAGAAATTAATGCC 2160
Db 2101 CCTACCTTGTGGAGGTGACAGTTTCTCATGTAAGAGCTGCAGAAAGAAATTAATGCC 2160
Qy 2161 GCGCACTTAAACCCAGTGTGAAAGAAAGAAATTAACCATTTTGAAGATTTGTGCG 2220
Db 2161 GCGCACTTAAACCCAGTGTGAAAGAAAGAAATTAACCATTTTGAAGATTTGTGCG 2220
Qy 2221 AGCATCCCTTAAAGGCACTCTCCAGAGCTCTCTCATGATGATCAGAGCTGAGCT 2280
Db 2221 AGCATCCCTTAAAGGCACTCTCCAGAGCTCTCTCATGATGATCAGAGCTGAGCT 2280
Qy 2281 CCCCCAAGCCGAGTCTTCCAGAGCTCTCTCATGATGATCAGAGCTGAGCTGAGCT 2340
Db 2281 CCCCCAAGCCGAGTCTTCCAGAGCTCTCTCATGATGATCAGAGCTGAGCTGAGCT 2340
Qy 2341 GCTCTGCTTCCCTGTAATCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Db 2341 GCTCTGCTTCCCTGTAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Qy 2401 CCGAAGAGGAAATGAGAGGAGAACTAGTCTTAAGAGAAATCTGAGAGGAGAGAGT 2460
Db 2401 CCGAAGAGGAAATGAGAGGAGAACTAGTCTTAAGAGAAATCTGAGAGGAGAGAGT 2460
Qy 2461 CTCAGAGGAGAAAGGGGCTTCCAGCTCCAGAGAAATTCAGAGGTGGAGCTGCAGAG 2520
Db 2461 CTCAGAGGAGAAAGGGGCTTCCAGCTCCAGAGAAATTCAGAGGTGGAGCTGCAGAG 2520
Qy 2521 TGGGAGCGCTGAGGCTGAGGAGGTGTGAAAGAGAGAGAGAGTGAAGAGGCTGA 2580
Db 2521 TGGGAGCGCTGAGGCTGAGGAGGTGTGAAAGAGAGAGAGAGTGAAGAGGCTGA 2580
Qy 2581 GCTGCCAGATGTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
Db 2581 GCTGCCAGATGTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640

Db 2581 GCTGCCAGATGTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
Qy 2641 CTTTATATCTTCTCTGCTGGAGAGAGAGTCTATTTTCAAGAGGATGAGTTTC 2700
Db 2641 CTTTATATCTTCTCTGCTGGAGAGAGAGTCTATTTTCAAGAGGATGAGTTTC 2700
Qy 2701 ATAAAGTCACTGTAAATTCAGAGGTGTGATGAGGTGTGTGTGTGTGTGTGTGT 2760
Db 2701 ATAAAGTCACTGTAAATTCAGAGGTGTGATGAGGTGTGTGTGTGTGTGTGTGT 2760
Qy 2761 TTAATGGGAATATAGGAAGGAGCTCAATTCCTGAGGCGCTTAATTCAGGAAGAGT 2820
Db 2761 TTAATGGGAATATAGGAAGGAGCTCAATTCCTGAGGCGCTTAATTCAGGAAGAGT 2820
Qy 2821 TGAAGTCTTCTTCTCATGCTCTTCTGGGCACTACTCAGCCCTGTGTGACTTGTG 2880
Db 2821 TGAAGTCTTCTTCTCATGCTCTTCTGGGCACTACTCAGCCCTGTGTGACTTGTG 2880
Qy 2881 TGCAAGAGGTGAGAAACCTTGGAATCAGAGAGTGTGTGTGTGTGTGTGTGTGTGT 2940
Db 2881 TGCAAGAGGTGAGAAACCTTGGAATCAGAGAGTGTGTGTGTGTGTGTGTGTGTGT 2940
Qy 2941 GGTGTGCTGTGCAACCGTGGCAAGTGTCTCTCTTCCCTGGGCACTAGTCTTCTGT 3000
Db 2941 GGTGTGCTGTGCAACCGTGGCAAGTGTCTCTCTTCCCTGGGCACTAGTCTTCTGT 3000
Qy 3001 ATAAAGACCTTGTGAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
Db 3001 ATAAAGACCTTGTGAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
Qy 3061 GATGCTTGAAGGGGAAAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3120
Db 3061 GATGCTTGAAGGGGAAAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3120
Qy 3121 GAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3180
Db 3121 GAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3180
Qy 3181 CAGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240
Db 3181 CAGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240
Qy 3241 TCCCTAAGCATATGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3300
Db 3241 TCCCTAAGCATATGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3300
Qy 3301 GGTAGCTTTTCCCTGAGATTTCAAAAATCTGGGCGAGAGCAAGTGTGAAGAGTGT 3360
Db 3301 GGTAGCTTTTCCCTGAGATTTCAAAAATCTGGGCGAGAGCAAGTGTGAAGAGTGT 3360
Qy 3361 TTAACCTTTTCAACCTGAGCAGACCCAGCAGCTCAGCAGTGTGTGTGTGTGTGTGT 3420
Db 3361 TTAACCTTTTCAACCTGAGCAGACCCAGCAGCTCAGCAGTGTGTGTGTGTGTGTGT 3420
Qy 3421 AGTACCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3480
Db 3421 AGTACCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3480
Qy 3481 ACAGATTCATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3540
Db 3481 ACAGATTCATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3540
Qy 3541 GTTCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3600
Db 3541 GTTCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3600
Qy 3601 CCGATTTCTTAATCAATATATTTTCTTTTCAAGGAGTGTGTGTGTGTGTGTGTGTGT 3660
Db 3601 CCGATTTCTTAATCAATATATTTTCTTTTCAAGGAGTGTGTGTGTGTGTGTGTGTGT 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 3720
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Db 4140 TTATATGGCTATTGGCACTTGGTTTTGTTTTTCTCTTGGGTTTATTAAGTAAACA 4139
Qy 4200 GGGATTTTAACTTACAGTCCAGAAAGCTTGGAATTGAATGAGCAAAAATTACATTT 4259
Db 4200 GGGATTTTAACTTACAGTCCAGAAAGCTTGGAATTGAATGAGCAAAAATTACATTT 4259
Qy 4260 TTGTTTTTACACCTTCATTAATAATTAACTTTATTCATTCGATGAGGACATTA 4319
Db 4260 TTGTTTTTACACCTTCATTAATAATTAACTTTATTCATTCGATGAGGACATTA 4319
Qy 4320 ACTCAAGTGTAAATAACAGTACCTGTGATTTTGTCAATTCACATTAAGAAATCAAGACAT 4379
Db 4320 ACTCAAGTGTAAATAACAGTACCTGTGATTTTGTCAATTCACATTAAGAAATCAAGACAT 4379
Qy 4380 TTATATCTATATATACAGTGTGAGATACGTTGTAAGGAAATTTATCTGAAAAT 4439
Db 4380 TTATATCTATATATACAGTGTGAGATACGTTGTAAGGAAATTTATCTGAAAAT 4439
Qy 4440 ACTTGAATTTAGACCTCTGCTGATCTGTTTAAATATTAATAAATCATGTTAA 4499
Db 4440 ACTTGAATTTAGACCTCTGCTGATCTGTTTAAATATTAATAAATCATGTTAA 4499
Qy 4500 AATTGTGAATTTGATATATATATATATATATATATATATATATATATATATATAT 4559
Db 4500 AATTGTGAATTTGATATATATATATATATATATATATATATATATATATATATAT 4559
Qy 4560 TATATATTTGAAAAATCTTTCTGAGAAAGTCCAGATTTCCACATAGAGGTTCTTG 4619
Db 4560 TATATATTTGAAAAATCTTTCTGAGAAAGTCCAGATTTCCACATAGAGGTTCTTG 4619
Qy 4620 GCATGACACACACAGATTAATACTGATTTAGAGGCTTACATGACATTTGAGGCTGAG 4679
Db 4620 GCATGACACACACAGATTAATACTGATTTAGAGGCTTACATGACATTTGAGGCTGAG 4679
Qy 4680 ATGCAAGCTGAAATTAAGAAAGTTCTCCCAAGATACACATTTTAAAGTAAAGGGGT 4739
Db 4680 ATGCAAGCTGAAATTAAGAAAGTTCTCCCAAGATACACATTTTAAAGTAAAGGGGT 4739
Qy 4740 GAGGGGGGAAATCTGCGCTCTATAGGAATGCTCTCCCTGAGAGGCTGAGGCTGCT 4799
Db 4740 GAGGGGGGAAATCTGCGCTCTATAGGAATGCTCTCCCTGAGAGGCTGAGGCTGCT 4799
Qy 4800 CCTTGATTTCTGCGCTGCTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859
Db 4800 CCTTGATTTCTGCGCTGCTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859
Qy 4860 TGGATCTCAGTTCCTAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4919
Db 4860 TGGATCTCAGTTCCTAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4919
Qy 4920 GTGATGGAATATTAATACTAATAATATATCTTGTGAAATTCAGACACCAAGTCTTG 4979
Db 4920 GTGATGGAATATTAATACTAATAATATATCTTGTGAAATTCAGACACCAAGTCTTG 4979
Qy 4980 GTTAAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5039
Db 4980 GTTAAAGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5039
Qy 5040 ATAGGAATCTATTTATGAGGTATGAGTCAATAATGGAGTGTCTTTTAAAAAGAACT 5099
Db 5040 ATAGGAATCTATTTATGAGGTATGAGTCAATAATGGAGTGTCTTTTAAAAAGAACT 5099
Qy 5100 CCAAAAGACTTCTGGAAGTTATTTCTTAAAGATCTGCTGACAGGAGGAGGACACC 5159
Db 5100 CCAAAAGACTTCTGGAAGTTATTTCTTAAAGATCTGCTGACAGGAGGAGGACACC 5159
Qy 5160 CCTGTGTACAGCCCCACCAAGCTTCAAGTGGCCACCTGTGTTTCCCATGAAGGGCT 5219
Db 5160 CCTGTGTACAGCCCCACCAAGCTTCAAGTGGCCACCTGTGTTTCCCATGAAGGGCT 5219
Qy 5220 GGCTCCCAAGATATATAAAGCTCTCTGAGGCTGGGCAATGAGCCGCAAG 5271

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Db 5220 GGCTCCCAAGATATATAAAGCTCTCTGAGGCTGGGCAATGAGCCGCAAG 5271
RESULT 9
AAV51366
ID AAV51366 standard; DNA; 5300 BP.
XX
AC AAV51366;
XX
DE 27-OCT-1998 (first entry)
XX
DE Human TIGR promoter mutant TIGRm5 DNA.
XX
KW TIGR; trabecular meshwork induced glucocorticoid response protein; human;
diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation 4262
FT /tag= a
FT /note= "Wild-type G is replaced with A"
XX
PN WO9832850-A1.
XX
PD 30-JUL-1998.
XX
PF 09-JAN-1998; 98MO-US000468.
XX
PR 28-JAN-1997; 97US-00791154.
PR 26-SEP-1997; 97US-00938669.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Nguyen TD, Polansky JR, Chen P, Chen H;
XX
DR WPI; 1998-427946/36.
XX
PT Use of TIGR nucleic acid sequences - used for, e.g. developing products
for diagnosis, prognosis and treatment of glaucoma.
XX
PS Disclosure; Fig 2; 105pp; English.
XX
CC This sequence is a trabecular meshwork induced glucocorticoid response
protein (TIGR) promoter mutant, TIGRm5, which is used in a method for
diagnosing glaucoma in a patient. The method involves the detection of
CC polymorphisms whose presence is predictive of a mutation affecting TIGR
response in the patient and can be diagnostic of glaucoma or steroid
CC sensitivity. Base substitutions and base additions upstream of and within
TIGR exons can also be used to diagnose glaucoma
XX
SQ Sequence 5300 BP; 1483 A; 1152 C; 1234 G; 1431 T; 0 U; 0 Other;
Query Match 99.5%; Score 5244.8; DB 2; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5268; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
Qy 1 ATCTTGTTCAGTTTACCTCAGGCTATTTATGAATGAATGAGATTAACCAATGGAAG 60
Db 1 ATCTTGTTCAGTTTACCTCAGGCTATTTATGAATGAATGAGATTAACCAATGGAAG 60
Qy 61 TCCATTAATACTGATATAGCCTTCATTTGGATGATGTCTTTTGGCAGATGATPAAAGATCA 120
Db 61 TCCATTAATACTGATATAGCCTTCATTTGGATGATGTCTTTTGGCAGATGATPAAAGATCA 120
Qy 121 GGAAGAAGAGTATCCACCTTAGCCCAAGTGCACAGGCTGTGCTCTTATTTTAAAGGA 180
Db 121 GGAAGAAGAGTATCCACCTTAGCCCAAGTGCACAGGCTGTGCTCTTATTTTAAAGGA 180
Qy 181 CAGATGTGCTCTCTGACAGAACCTATTTCTTCAAGAAATCAATCAATCAATATGTTAAATC 240
Db 181 CAGATGTGCTCTCTGACAGAACCTATTTCTTCAAGAAATCAATCAATCAATATGTTAAATC 240

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Qy 241 CATCAACAGAGCTAAGAAACAGAAATGATGGCACTTGCCCAAGAAAAATGCCAG 300  
 Db 241 CATCAACAGAGCTAAGAAACAGAAATGATGGCACTTGCCCAAGAAAAATGCCAG 300  
 Qy 301 GAGAGCAATATATGATGAAAAATTAATCTTCCCTTGTTTAAATTTTCAAGAAAAATG 360  
 Db 301 GAGAGCAATATATGATGAAAAATTAATCTTCCCTTGTTTAAATTTTCAAGAAAAATG 360  
 Qy 361 ATGAGGACCAAAATCAATGAAATAGAAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG 420  
 Db 361 ATGAGGACCAAAATCAATGAAATAGAAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG 420  
 Qy 421 TAATTAAGTATTTGTTCTTGAGAAAGACCTCCAGATGAGCTGATGGGAAAAATGGAA 480  
 Db 421 TAATTAAGTATTTGTTCTTGAGAAAGACCTCCAGATGAGCTGATGGGAAAAATGGAA 480  
 Qy 481 AAACGTCAAAAGATGATCTGATCAGATCCCAAGTGAATTAATTTTAAAAACAGAT 540  
 Db 481 AAACGTCAAAAGATGATCTGATCAGATCCCAAGTGAATTAATTTTAAAAACAGAT 540  
 Qy 541 GGCATCACTCTGGGAGGCAAGTTCAAGAAAGTCATGTTAGCAAAAGATATAAATTAAC 600  
 Db 541 GGCATCACTCTGGGAGGCAAGTTCAAGAAAGTCATGTTAGCAAAAGATATAAATTAAC 600  
 Qy 601 AGCAAAATCAAAATTCGCAAAATGCAAGAAATGGGGAATGGGGAATGGGGAATGGGGA 660  
 Db 601 AGCAAAATCAAAATTCGCAAAATGCAAGAAATGGGGAATGGGGAATGGGGAATGGGGA 660  
 Qy 661 AGTATTAGSCAGTGTGACATGTTGCAACACCTCCGCTTATACAGGAAACCAAA 720  
 Db 661 AGTATTAGSCAGTGTGACATGTTGCAACACCTCCGCTTATACAGGAAACCAAA 720  
 Qy 721 ATTGACTGGGCTAAGCCTGACCTTCAAGGAAATATGAAAAATCTAGAGCAAAACAAA 780  
 Db 721 ATTGACTGGGCTAAGCCTGACCTTCAAGGAAATATGAAAAATCTAGAGCAAAACAAA 780  
 Qy 781 GACATGTTTAAAGGCAACCAAGAAATGTCAGACCTTCAAGAGCAAGTCCCTCAGCA 840  
 Db 781 GACATGTTTAAAGGCAACCAAGAAATGTCAGACCTTCAAGAGCAAGTCCCTCAGCA 840  
 Qy 841 GGGACCTGAGGCAATTTGCTTTAGAGAGCCAGTTTCTTAAAGAAATCTTAAAGAACTC 900  
 Db 841 GGGACCTGAGGCAATTTGCTTTAGAGAGCCAGTTTCTTAAAGAAATCTTAAAGAACTC 900  
 Qy 901 TTGAAAGATCATGAATTTTAAACATTTTAAAGTAAATCAAAATATGCAATGATACG 960  
 Db 901 TTGAAAGATCATGAATTTTAAACATTTTAAAGTAAATCAAAATATGCAATGATACG 960  
 Qy 961 TTTAGACATGGTCCCAATTTTAAAGTCAAGGCAATPACAGATTAAGTGTCCAGCTCC 1020  
 Db 961 TTTAGACATGGTCCCAATTTTAAAGTCAAGGCAATPACAGATTAAGTGTCCAGCTCC 1020  
 Qy 1021 GGAATGGTCAAGAAATCTTGAATCACTGTGTCCTCCATCTTAACTTTTCAAGATGATC 1080  
 Db 1021 GGAATGGTCAAGAAATCTTGAATCACTGTGTCCTCCATCTTAACTTTTCAAGATGATC 1080  
 Qy 1081 TGTCTAAGCCCTCACAACAGAGCCCAATGTGTCTGACCTTAAACCAATCTTAAACCAA 1140  
 Db 1081 TGTCTAAGCCCTCACAACAGAGCCCAATGTGTCTGACCTTAAACCAATCTTAAACCAA 1140  
 Qy 1141 GTGCTCAACATTTGTTAAAGTGTCAATCTGATAGGTCATTAAGCAAGTCCCTCC 1200  
 Db 1141 GTGCTCAACATTTGTTAAAGTGTCAATCTGATAGGTCATTAAGCAAGTCCCTCC 1200  
 Qy 1201 TGTGAGCCCATCCCGCTCCACAGGAAGTCTCCCACTTAAAGTCTTAAAGTCTTAA 1260  
 Db 1201 TGTGAGCCCATCCCGCTCCACAGGAAGTCTCCCACTTAAAGTCTTAAAGTCTTAA 1260  
 Qy 1261 TACAGCCGAAGCTCCGTGAGGGTGTGTCTTACACCTTACCTGTATGCTTAC 1320  
 Db 1261 TACAGCCGAAGCTCCGTGAGGGTGTGTCTTACACCTTACCTGTATGCTTAC 1320

Qy 1321 ACCTGAGCTCAGTCAACCTCTGCTCCAGGTTCAAGAAATTTCTGTCAGGCTCC 1380  
 Db 1321 ACCTGAGCTCAGTCAACCTCTGCTCCAGGTTCAAGAAATTTCTGTCAGGCTCC 1380  
 Qy 1381 CGCGTAGCTGGACATACAGAGCCGACAGCCCGCTAATTTTGTATTTAGTATGATGGG 1440  
 Db 1381 CGCGTAGCTGGACATACAGAGCCGACAGCCCGCTAATTTTGTATTTAGTATGATGGG 1440  
 Qy 1441 GTTTCACATATTAAGCCCGGCTGTGTGAACTCTGACCTGAGTGTATCCACCACTC 1500  
 Db 1441 GTTTCACATATTAAGCCCGGCTGTGTGAACTCTGACCTGAGTGTATCCACCACTC 1500  
 Qy 1501 AGCCTCTTAAAGTGTGGGATTAACAGGATGAGTACCGCGCCGCAAGGATCAGTGT 1560  
 Db 1501 AGCCTCTTAAAGTGTGGGATTAACAGGATGAGTACCGCGCCGCAAGGATCAGTGT 1560  
 Qy 1561 TTAATTAAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
 Db 1561 TTAATTAAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
 Qy 1621 TTAATTAAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
 Db 1621 TTAATTAAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
 Qy 1681 CACTGCTCTCATCACTTCTTCCCTCATCTCATCTTCAAGGCTAAGTTACATTTAAT 1740  
 Db 1681 CACTGCTCTCATCACTTCTTCCCTCATCTCATCTTCAAGGCTAAGTTACATTTAAT 1740  
 Qy 1741 CACCATGCTTTTGTGTATGAGCTTCCCATGCTTCAAGGATGATGATGATGATGATGAT 1800  
 Db 1741 CACCATGCTTTTGTGTATGAGCTTCCCATGCTTCAAGGATGATGATGATGATGATGAT 1800  
 Qy 1801 TTCCATTTGGGAGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860  
 Db 1801 TTCCATTTGGGAGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860  
 Qy 1861 TGAAGCCCCCGGCAAGGATTTCTCTCCAGCTGAGGAGGACCTGCAAGCAACCCGGGCTC 1920  
 Db 1861 TGAAGCCCCCGGCAAGGATTTCTCTCCAGCTGAGGAGGACCTGCAAGCAACCCGGGCTC 1920  
 Qy 1921 TGGGTGTCTGAGCAACCTGCAAGCCGAGCACTGCTGTTTGTATCACTCTCTAG 1980  
 Db 1921 TGGGTGTCTGAGCAACCTGCAAGCCGAGCACTGCTGTTTGTATCACTCTCTAG 1980  
 Qy 1981 GACCTGTGCTTCTAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
 Db 1981 GACCTGTGCTTCTAATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
 Qy 2041 TATTGAGTACTTATCTGCGCAACCAAGAAATGAGGAAATGAGGAAATGAGGAAATGAG 2100  
 Db 2041 TATTGAGTACTTATCTGCGCAACCAAGAAATGAGGAAATGAGGAAATGAGGAAATGAG 2100  
 Qy 2101 CTAACCTGTGAGAGTGAACAGTTTCTCATGGAAGCTGAGGAAATGAGGAAATGAGGAA 2160  
 Db 2101 CTAACCTGTGAGAGTGAACAGTTTCTCATGGAAGCTGAGGAAATGAGGAAATGAGGAA 2160  
 Qy 2161 GCGAATTTAAACCAAGTGTGAAAGAAAGAAATTAACCAATTTTGAAGAAATTTGTGGC 2220  
 Db 2161 GCGAATTTAAACCAAGTGTGAAAGAAAGAAATTAACCAATTTTGAAGAAATTTGTGGC 2220  
 Qy 2221 AGCATCTCTTAAAGGCAACCTCCTTACGCGCCCTGCTGCTCATGTCGCGGAGG 2280  
 Db 2221 AGCATCTCTTAAAGGCAACCTCCTTACGCGCCCTGCTGCTCATGTCGCGGAGG 2280  
 Qy 2281 CCCCCAAGCCGAGTCTTCCAGAGCTCTCTCATCAAGTCAACAGGCTGACGCTGCT 2340  
 Db 2281 CCCCCAAGCCGAGTCTTCCAGAGCTCTCTCATCAAGTCAACAGGCTGACGCTGCT 2340  
 Qy 2341 GCGTGTCTCCGAGT 2400  
 Db 2341 GCGTGTCTCCGAGT 2400  
 Qy 2401 CCAAGAAAGAAATGAGAGGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2460

Db 2401 CCGAAGAGAAATGAGAGGAAACTAGCTTAACGAGAAATCTGGAGGGGACAGTGTTC 2460  
Qy 2461 CTAGAGGAGAAAGGGGCTCCAGCTCCAGAGAAATTCAGAGGAGTGGAGGAG 2520  
Db 2461 CTAGAGGAGAAAGGGGCTCCAGCTCCAGAGAAATTCAGAGGAGTGGAGGAG 2520  
Qy 2521 TGGGAGCGCTGGGGCTGAGCGGCTGTGAAGAGCAGAAAGGTGAAGGGGCAAGGCTGAA 2580  
Db 2521 TGGGAGCGCTGGGGCTGAGCGGCTGTGAAGAGCAGAAAGGTGAAGGGGCAAGGCTGAA 2580  
Qy 2581 GCTGCCAGATGTGAGTGTGTTCACGGGGCTGGAGATTTCCGTTGCTTCCTGAGC 2640  
Db 2581 GCTGCCAGATGTGAGTGTGTTCACGGGGCTGGAGATTTCCGTTGCTTCCTGAGC 2640  
Qy 2641 CTTTATCTTTTCTCTGCTTGAAGAGAAAGTCTATTCAATGAAGGATGCAATTC 2700  
Db 2641 CTTTATCTTTTCTCTGCTTGAAGAGAAAGTCTATTCAATGAAGGATGCAATTC 2700  
Qy 2701 ATAAATCAGCTTTAAATTCAGAGGTGTGATGGTTCCTTCAGAGGCTTAT 2760  
Db 2701 ATAAATCAGCTTTAAATTCAGAGGTGTGATGGTTCCTTCAGAGGCTTAT 2760  
Qy 2761 TTAATGGAAATATAGAGACGAGCTATTCTTAGCCGTTAATTCAGAGAAAGTAC 2820  
Db 2761 TTAATGGAAATATAGAGACGAGCTATTCTTAGCCGTTAATTCAGAGAAAGTAC 2820  
Qy 2821 TGAAGTCTTTCTTCATGTCTTCGGGCACTACAGCCCTGGTGAATTCGCTTA 2880  
Db 2821 TGAAGTCTTTCTTCATGTCTTCGGGCACTACAGCCCTGGTGAATTCGCTTA 2880  
Qy 2881 TGAAGTCTTTCTTCATGTCTTCGGGCACTACAGCCCTGGTGAATTCGCTTA 2880  
Db 2881 TGAAGTCTTTCTTCATGTCTTCGGGCACTACAGCCCTGGTGAATTCGCTTA 2880  
Qy 2941 GGTGGCTGTGAGCGTGGGCAAGTGTCTCTTCCCTGGGCAATGCTTCTGCT 3000  
Db 2941 GGTGGCTGTGAGCGTGGGCAAGTGTCTCTTCCCTGGGCAATGCTTCTGCT 3000  
Qy 3001 ATAAAGACCTTGACGCTCTGCTGTCTGTGAACACTCCCTGATTCCTGTGAGAGG 3060  
Db 3001 ATAAAGACCTTGACGCTCTGCTGTCTGTGAACACTCCCTGATTCCTGTGAGAGG 3060  
Qy 3061 GGAATGTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120  
Db 3061 GGAATGTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120  
Qy 3121 GGAAG 3180  
Db 3121 GGAAG 3180  
Qy 3181 CAGGACCGAGAGCCCAATGCTTCAGAAAGCTCAATGAACCAACAGCACAATTTCT 3240  
Db 3181 CAGGACCGAGAGCCCAATGCTTCAGAAAGCTCAATGAACCAACAGCACAATTTCT 3240  
Qy 3241 TCCCTAAGCATAGACATGCAATTTGCCAATTAACCAAAAGATGACAGACTGCT 3300  
Db 3241 TCCCTAAGCATAGACATGCAATTTGCCAATTAACCAAAAGATGACAGACTGCT 3300  
Qy 3301 GGTAGCTTTGCTGCTGCAATTAACCAAAAGCTGGGCAAGAGAGAGAGAGAGAG 3360  
Db 3301 GGTAGCTTTGCTGCTGCAATTAACCAAAAGCTGGGCAAGAGAGAGAGAGAGAG 3360  
Qy 3361 TTAATCTTTTCACTGACAGACCCAGCAGCTGACAGTGAAGAGAGAGAGAGAG 3420  
Db 3361 TTAATCTTTTCACTGACAGACCCAGCAGCTGACAGTGAAGAGAGAGAGAGAG 3420  
Qy 3421 AGTGAAGTGAAG 3480  
Db 3421 AGTGAAGTGAAG 3480  
Qy 3481 ACAGATTCATTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540  
Db 3481 ACAGATTCATTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540

Db 3481 ACAGATTCATTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540  
Qy 3541 GTTCAG 3600  
Db 3541 GTTCAG 3600  
Qy 3601 CCTGATTTCTAATACATATATTTTCTTTCATACAGAGTGAATTTGAGAGAGTCAAG 3660  
Db 3601 CCTGATTTCTAATACATATATTTTCTTTCATACAGAGTGAATTTGAGAGAGTCAAG 3660  
Qy 3661 GTAGAACTGAGAGCTGAAGATTAAGTGTCTGCTTATTAAGAACTCTTTCTCTG 3720  
Db 3661 GTAGAACTGAGAGCTGAAGATTAAGTGTCTGCTTATTAAGAACTCTTTCTCTG 3720  
Qy 3721 GGAATTAAG 3780  
Db 3721 GGAATTAAG 3780  
Qy 3781 TAAAGCCAAACAGATTAAGAGCTGAGTCTTGAGCTGACATATGATGGTGTGAAAT 3840  
Db 3781 TAAAGCCAAACAGATTAAGAGCTGAGTCTTGAGCTGACATATGATGGTGTGAAAT 3840  
Qy 3841 CATTCAGAGATGTTACTATCTGATTCAGAAAATGAGACTAGTACCTTGTGAGCTG 3900  
Db 3841 CATTCAGAGATGTTACTATCTGATTCAGAAAATGAGACTAGTACCTTGTGAGCTG 3900  
Qy 3901 TTAACAAACACCGAGTGTAAATGCTCAAGTCAAGCTTAAGTGAAGAGAGAGAGAG 3959  
Db 3901 TTAACAAACACCGAGTGTAAATGCTCAAGTCAAGCTTAAGTGAAGAGAGAGAGAG 3959  
Qy 3961 TAAACAAACACCGAGTGTAAATGCTCAAGTCAAGCTTAAGTGAAGAGAGAGAGAG 3960  
Db 3961 TAAACAAACACCGAGTGTAAATGCTCAAGTCAAGCTTAAGTGAAGAGAGAGAGAG 3960  
Qy 3961 TAAACAAACACCGAGTGTAAATGCTCAAGTCAAGCTTAAGTGAAGAGAGAGAGAG 3960  
Db 3961 TAAACAAACACCGAGTGTAAATGCTCAAGTCAAGCTTAAGTGAAGAGAGAGAGAG 3960  
Qy 4020 CAGTTGGAAATATTTACTTCAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4079  
Db 4020 CAGTTGGAAATATTTACTTCAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4079  
Qy 4080 TTGCTCAAGAGCAATTAATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTGGTATA 4139  
Db 4080 TTGCTCAAGAGCAATTAATTTCAAGTGGCTTAAAGTACTTCTGACAGTTTGGTATA 4139  
Qy 4140 TTTATGAGATTCAGATTTGCTTTTGTGTTTCTTCTTGGGTTTATTAATGTAAGCA 4199  
Db 4140 TTTATGAGATTCAGATTTGCTTTTGTGTTTCTTCTTGGGTTTATTAATGTAAGCA 4199  
Qy 4200 GGAATTAATTAAGTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4259  
Db 4200 GGAATTAATTAAGTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4259  
Qy 4260 TTAATTTTACACCTTCAACTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 4319  
Db 4260 TTAATTTTACACCTTCAACTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 4319  
Qy 4320 ACTCAAGTGTATTAAGTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4379  
Db 4320 ACTCAAGTGTATTAAGTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4379  
Qy 4380 TTTATCTAATTAAGTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4439  
Db 4380 TTTATCTAATTAAGTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4439  
Qy 4440 ACTTGAATTAAGAGCTGCTGCTGAGATCTTGTGTTTAAACATTAATTAATTAATTA 4499  
Db 4440 ACTTGAATTAAGAGCTGCTGCTGAGATCTTGTGTTTAAACATTAATTAATTAATTAAT 4499  
Qy 4500 AATTTGATTAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4559  
Db 4500 AATTTGATTAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4559  
Qy 4560 TATAATTTGAAAAATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4619  
Db 4560 TATAATTTGAAAAATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4619

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	RESULT 10
AAV5_1362	
ID	AAV51362 standard; DNA; 5300 BP.
XX	
AC	AAV51362;
XX	
DT	27-OCT-1998 (first entry)
XX	
DE	Human TIGR promoter mutant TIGRmt1 DNA.
XX	
KW	TIGR; trabecular meshwork induced glucocorticoid response protein; human
KX	diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
FH	Key
FT	mutation
FT	Location/Qualifiers
XX	4337
XX	/tag= a
FN	/note= "Wild type C is replaced by G"
PD	
PD	30-JUL-1998.
PF	
PF	09-JAN-1998; 98MO-US000468.
XX	

CC This sequence is a trabecular meshwork induced glucocorticoid response  
CC protein (TIGR) promoter mutant, TIGRmt1, which is used in a method for  
CC diagnosing glaucoma in a patient. The method involves the detection of  
CC polymorphisms whose presence is predictive of a mutation affecting TIGR  
CC response in the patient and can be diagnostic of glaucoma or steroid  
CC sensitivity. Base substitutions and base additions upstream of and within  
CC TIGR exons can also be used to diagnose glaucoma

XX  
SQ Sequence 5300 BP; 1482 A; 1151 C; 1236 G; 1431 T; 0 U; 0 Other;

Query Match 99.5%; Score 5244.8; DB 2; Length 5300;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5268; Conservative 0; Mismatches 2; Indels 2; Gaps 2

Qy	1	ATTCTTGTCAGATTACCTCAGGGGCTATTATGAATGAATGAAATACCAATGCGAAG	60
Dp	1	ATTCTTGTCAGATTACCTCAGGGGCTATTATGAATGAATGAAATACCAATGCGAAG	60
Qy	61	TCTCTAATACTGATAGCTCCATTCGGATGATGCTTTGGCAGATGATAAAGATCA	120
Dp	61	TCTCTAATACTGATAGCTCCATTCGGATGATGCTTTGGCAGATGATAAAGATCA	120
Qy	121	GGAGAAGAGATACCTCAGGTTAGCCCAATGTCCAGGCTGTGTCTGCTTATTTTAGTGA	180
Dp	121	GGAGAAGAGATACCTCAGGTTAGCCCAATGTCCAGGCTGTGTCTGCTTATTTTAGTGA	180
Qy	181	CAGATCTGCTCCTGACGAGAGCTATTCTTAGAATAATCACAATCCAAATGGTAATC	240
Dp	181	CAGATCTGCTCCTGACGAGAGCTATTCTTAGAATAATCACAATCCAAATGGTAATC	240
Qy	241	CATCAAAACAGAGCTAAGAAAACAGGAATGAGATGGGCACTTGCCCAAGAAAAATGCGAG	300
Dp	241	CATCAAAACAGAGCTAAGAAAACAGGAATGAGATGGGCACTTGCCCAAGAAAAATGCGAG	300
Qy	301	GAGAGCAATATATGATGAAAAATGAACTTTCCCTTTGTTTATTTTCAGAAAAAATG	360
Dp	301	GAGAGCAATATATGATGAAAAATGAACTTTCCCTTTGTTTATTTTCAGAAAAAATG	360
Qy	361	ATGAGAGCCAAATCAATGAAATAGAAAAACAGCTCAGAAAAAAGATGTTCCAAATGG	420
Dp	361	ATGAGAGCCAAATCAATGAAATAGAAAAACAGCTCAGAAAAAAGATGTTCCAAATGG	420
Qy	421	TAAATTAAGATTTGTTCCCTGGGAGAAACCTCCATGTGAGCTTGAGGGGAAATGGGAA	480
Dp	421	TAAATTAAGATTTGTTCCCTGGGAGAAACCTCCATGTGAGCTTGAGGGGAAATGGGAA	480
Qy	481	AAAAGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCGAT	540
Dp	481	AAAAGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCGAT	540
Qy	541	GGCATACACTCTGGGAGGCAAGTTACAGAAAGTCAATGTATGCAAAAGACATAACAAATPAC	600
Dp	541	GGCATACACTCTGGGAGGCAAGTTACAGAAAGTCAATGTATGCAAAAGACATAACAAATPAC	600
Qy	601	AGCAAAATCAAAATTTCCGCAAAATGACAGAGAAAAATGGGACTGGGAAAACCTTCATPAC	660
Dp	601	AGCAAAATCAAAATTTCCGCAAAATGACAGAGAAAAATGGGACTGGGAAAACCTTCATPAC	660
Qy	661	AGGATTTAGGCAATTGACCATGTTTGGCAACACTCCCGCTTATATACAGGAAACACAAA	720

Db 661 AGGATTTAGGAGGTTGACCATGTTGGCAACGCTCCCGTCTATACCGAGGGAACACAAA 720  
Qy 721 ATTGACTGGGCTTAAGCTGTGACTTTCAAGGGAATATGAAAACGTGAGAGAAAACAAA 780  
Db 721 ATTGACTGGGCTTAAGCTGTGACTTTCAAGGGAATATGAAAACGTGAGAGAAAACAAA 780  
Qy 781 GACATGTTAAAGGCAACCAAGCATGTGAGCTTCAAGAGCAGAGTGCCTTCAGCA 840  
Db 781 GACATGTTAAAGGCAACCAAGCATGTGAGCTTCAAGAGCAGAGTGCCTTCAGCA 840  
Qy 841 GGGACCTTGAGGCACTTGGCTTTAGGAAGGCGAGTTTCTTAAGAAATCTTAAGAAATCTC 900  
Db 841 GGGACCTTGAGGCACTTGGCTTTAGGAAGGCGAGTTTCTTAAGAAATCTTAAGAAATCTC 900  
Qy 901 TTGAAAGATCATGAATTTTAACTTTAAGTATGATTAAGCAAAATATGAGATGATTAACAG 960  
Db 901 TTGAAAGATCATGAATTTTAACTTTAAGTATGATTAAGCAAAATATGAGATGATTAACAG 960  
Qy 961 TTGAGCATGGGTCCCAATTTTAAAGTCAAGGCAATCAAGATTAACGTGTCCCAAGTCC 1020  
Db 961 TTGAGCATGGGTCCCAATTTTAAAGTCAAGGCAATCAAGATTAACGTGTCCCAAGTCC 1020  
Qy 1021 GGAATGCTGAGAAATCATTTAGAAATCACTGTGTCCCACTCTTAATTTTCAAGATGATC 1080  
Db 1021 GGAATGCTGAGAAATCATTTAGAAATCACTGTGTCCCACTCTTAATTTTCAAGATGATC 1080  
Qy 1081 TGTCAATGCTTCACACACAGGCGGATGTGTGACCTACACACAGATCTACACCCAA 1140  
Db 1081 TGTCAATGCTTCACACACAGGCGGATGTGTGACCTACACACAGATCTACACCCAA 1140  
Qy 1141 GTGCTCAACCTTTGTAACTGTATCTGATGATGCTCCCTTCAAAATGCCACTTCCC 1200  
Db 1141 GTGCTCAACCTTTGTAACTGTATCTGATGATGCTCCCTTCAAAATGCCACTTCCC 1200  
Qy 1201 TGTGACGAGGCTCCGCTCCACAGGAAGTCTCCCACTGATGATGATGATGATGATGAT 1260  
Db 1201 TGTGACGAGGCTCCGCTCCACAGGAAGTCTCCCACTGATGATGATGATGATGATGAT 1260  
Qy 1261 TACAGCCAGAACTCCGAGGAGGTGTGTCTTAACTTAACTTAACTTAACTTAACTTAA 1320  
Db 1261 TACAGCCAGAACTCCGAGGAGGTGTGTCTTAACTTAACTTAACTTAACTTAACTTAA 1320  
Qy 1321 AACTGAGCTCATGGAACCTCTGCTCCAGGTTCAAGCAATTCCTGTCTGAGCTCC 1380  
Db 1321 AACTGAGCTCATGGAACCTCTGCTCCAGGTTCAAGCAATTCCTGTCTGAGCTCC 1380  
Qy 1381 CGCGTAGCTGGAGCTACAGGCGCAGCCGAGCTAATTTTGTATTTGTATGTATGATGG 1440  
Db 1381 CGCGTAGCTGGAGCTACAGGCGCAGCCGAGCTAATTTTGTATTTGTATGTATGATGG 1440  
Qy 1441 GTTTACCTATTTAAGCCGCTGTGTGTGAATCTCTGATCTCAAGGTATCAACCCACTC 1500  
Db 1441 GTTTACCTATTTAAGCCGCTGTGTGTGAATCTCTGATCTCAAGGTATCAACCCACTC 1500  
Qy 1501 AACCTCTTAAAGTGTGGGATTTACAGGATGATCAAGCGCCCGGCAAGGCTCAGTGT 1560  
Db 1501 AACCTCTTAAAGTGTGGGATTTACAGGATGATCAAGCGCCCGGCAAGGCTCAGTGT 1560  
Qy 1561 TTAATTAAGGAATTAATTTGATTTTAACTTAACCAAGGGAACAGCAAAAGCTGTGA 1620  
Db 1561 TTAATTAAGGAATTAATTTGATTTTAACTTAACCAAGGGAACAGCAAAAGCTGTGA 1620  
Qy 1621 TAAATTAAGGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1680  
Db 1621 TAAATTAAGGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1680  
Qy 1681 CACTGCTCTATCACTTTCTCTCTCACTTTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCA 1740  
Db 1681 CACTGCTCTATCACTTTCTCTCTCACTTTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCA 1740  
Qy 1741 CACCATGCTTTGTGTAGGCTCCAGCATGTTCTGAAATTAAGATTAATTAAGTAACTAG 1800  
Db 1741 CACCATGCTTTGTGTAGGCTCCAGCATGTTCTGAAATTAAGATTAATTAAGTAACTAG 1800

Db 1741 CACCATGCTTTGTGTAGGCTCCAGCATGTTCTGAAATTAAGATTAATTAAGTAACTAG 1800  
Qy 1801 TTCAATTTGGGGGCACTGTGTGTGTATATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860  
Db 1801 TTCAATTTGGGGGCACTGTGTGTGTATATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860  
Qy 1861 TGAAGCCCGGAGAGGATTTCTCTCAGCTGGGGAGGCTTCAGAGCAACCGGGGCTC 1920  
Db 1861 TGAAGCCCGGAGAGGATTTCTCTCAGCTGGGGAGGCTTCAGAGCAACCGGGGCTC 1920  
Qy 1921 TGGGTGCTGAGAACCTGCAAGCCGCTGCACTGGTGTGTGTGTGTGTGTGTGTGTGTGT 1980  
Db 1921 TGGGTGCTGAGAACCTGCAAGCCGCTGCACTGGTGTGTGTGTGTGTGTGTGTGTGTGT 1980  
Qy 1981 GACCTGTGTCTTATTTCTGT 2040  
Db 1981 GACCTGTGTCTTATTTCTGT 2040  
Qy 2041 TATTGATTAATTAATTTCTGCAAGCAACCAAGCAAAATGTGTAGCAAGCACTGTCC 2100  
Db 2041 TATTGATTAATTAATTTCTGCAAGCAACCAAGCAAAATGTGTAGCAAGCACTGTCC 2100  
Qy 2101 CTTACCTTGTGAGGATGAGATTTCTCATGAGAGAGCTGCAAGAAATTAATAGCA 2160  
Db 2101 CTTACCTTGTGAGGATGAGATTTCTCATGAGAGAGCTGCAAGAAATTAATAGCA 2160  
Qy 2161 GCGAATTTAAACCAAGCTGCAAGAAAGAAATTAACCAATCTTGAAGATTTGTGCGC 2220  
Db 2161 GCGAATTTAAACCAAGCTGCAAGAAAGAAATTAACCAATCTTGAAGATTTGTGCGC 2220  
Qy 2221 AGCATGCTTTAAAGGCACTCCCTGAGGCGCCGCTGCTCATGATGATGATGATGATGATG 2280  
Db 2221 AGCATGCTTTAAAGGCACTCCCTGAGGCGCCGCTGCTCATGATGATGATGATGATGATG 2280  
Qy 2281 CCCCAGGAGGAGCTTCCAGGCTTCTCTCATGATGATGATGATGATGATGATGATGATG 2340  
Db 2281 CCCCAGGAGGAGCTTCCAGGCTTCTCTCATGATGATGATGATGATGATGATGATGATG 2340  
Qy 2341 GCTGCTGCTCCCGGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400  
Db 2341 GCTGCTGCTCCCGGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400  
Qy 2401 CCAGAAAGAAATGAGAGGAGAAATAGTCTAAAGGAGATGAGAGGAGGAGGAGGAGGAG 2460  
Db 2401 CCAGAAAGAAATGAGAGGAGAAATAGTCTAAAGGAGATGAGAGGAGGAGGAGGAGGAG 2460  
Qy 2461 CTCAGAGGAAAGGGGCTTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTTCAGAGG 2520  
Db 2461 CTCAGAGGAAAGGGGCTTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTTCAGAGG 2520  
Qy 2521 TGGGAGCGCTGGGCTGAGCGGCTGCTGAAAGGCAAGAGGTGAAGAGGCAAGGCTGGA 2580  
Db 2521 TGGGAGCGCTGGGCTGAGCGGCTGCTGAAAGGCAAGAGGTGAAGAGGCAAGGCTGGA 2580  
Qy 2581 GCTGCCAGATGTTCAAGTGTGTTCAAGGAGCTGAGAGGCTTCTGCTGCTGCTGCTGCTG 2640  
Db 2581 GCTGCCAGATGTTCAAGTGTGTTCAAGGAGCTGAGAGGCTTCTGCTGCTGCTGCTGCTG 2640  
Qy 2641 CTTTAACTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700  
Db 2641 CTTTAACTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700  
Qy 2701 AATAAGTCAAGTGTAAATTTCAAGGAGTGTGATGAGGATTTCTTCAAGAGGCTTTAT 2760  
Db 2701 AATAAGTCAAGTGTAAATTTCAAGGAGTGTGATGAGGATTTCTTCAAGAGGCTTTAT 2760  
Qy 2761 TTAATGGAATTAATGAGAGGAGTCAATTTCCAGAGGCTTTAATTAAGAGAGAGTGA 2820  
Db 2761 TTAATGGAATTAATGAGAGGAGTCAATTTCCAGAGGCTTTAATTAAGAGAGAGTGA 2820  
Qy 2821 TGAAGTCTTTCTTCACTGCTTCTGAGGCAACTACTCAGCCCTGTGTGTGTGTGTGTGTGT 2880  
Db 2821 TGAAGTCTTTCTTCACTGCTTCTGAGGCAACTACTCAGCCCTGTGTGTGTGTGTGTGTGT 2880

QY	288	TGCAAGAGGGTGA AAAACCTTGSAATAGAGACTGGATTTCTTTCTGGTTCGCAAT	2940
Db	2881	TGCAAGACGGTGGAAAACCTTGGAATCAGAGACTGGATTTCTTTCTGGTTCGCAAT	2940
QY	2941	GGTTGGCTGTGCGACCGTGGCAAGTGTCTCTCTCTCTGCGGCATATGCTTCTCTGCT	3000
Db	2941	GGTTGGCTGTGCGACCGTGGCAAGTGTCTCTCTCTCTGCGGCATATGCTTCTCTGCT	3000
QY	3001	ATTAAGACCCCTTGACGCTCTGTGATTCGTGAACACTTCCCTGTGATTCCTGTGAGGGG	3060
Db	3001	ATTAAGACCCCTTGACGCTCTGTGATTCGTGAACACTTCCCTGTGATTCCTGTGAGGGG	3060
QY	3061	GGATGTTGAGAGGGGAGAGAGAGCGACAGCTGGAGCAGTGAACCAAGGGAGGTGAGGG	3120
Db	3061	GGATGTTGAGAGGGGAGAGAGAGCGACAGCTGGAGCAGTGAACCAAGGGAGGTGAGGG	3120
QY	3121	GGACAGGAAGGCAAGGCAAGACTGGAGTGCCTCAATGCTCTCACTGATCAGCTCAGATC	3180
Db	3121	GGACAGGAAGGCAAGGCAAGACTGGAGTGCCTCAATGCTCTCACTGATCAGCTCAGATC	3180
QY	3181	CAGGACCGAGACCCAAATGCTTCAAGAAAGCTGCAATGAACCAACAGCCACATTTTCT	3240
Db	3181	CAGGACCGAGACCCAAATGCTTCAAGAAAGCTGCAATGAACCAACAGCCACATTTTCT	3240
QY	3241	TCCCTAAGCATGACAAATGGCATTGCGCAATTAACCAAAAAGATGAGAGACTAATCTGT	3300
Db	3241	TCCCTAAGCATGACAAATGGCATTGCGCAATTAACCAAAAAGATGAGAGACTAATCTGT	3300
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Db	3301	GGTAGCTTTGCTTGCCATTCAAAACTGGGCGCAGAGCAAGTGAAGAAAAGCCAGAGATTG	3360
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Db	3361	TTAAACTTTTCACTGACAGCAACCCCAAGCAGCTGACAGTGCCTGTCACAGACGG	3420
QY	3421	AGTGAAGCTGACGCGAGGGAGAGAGAGAAAAGAGGGATATGTGTATGACAGAAAG	3480
Db	3421	AGTGAAGCTGACGCGAGGGAGAGAGAGAAAAGAGGGATATGTGTATGACAGAAAG	3480
QY	3481	ACAGATTCAATCAAGGCGAGTGGGATTTGACCAAGGGAATTATGTCACAGTACCTGG	3540
Db	3481	ACAGATTCAATCAAGGCGAGTGGGATTTGACCAAGGGAATTATGTCACAGTACCTGG	3540
QY	3541	GTTCTTAGAGGCGAGGGCTATATGTTGGGGGGAAAAATCACTTCAAGGGAACTCGGAG	3600
Db	3541	GTTCTTAGAGGCGAGGGCTATATGTTGGGGGGAAAAATCACTTCAAGGGAACTCGGAG	3600
QY	3601	CCTGATTTCTAATATCTAATTTTCTTCAAGAGCTGAGTAATTTGACAGACTCAGAC	3660
Db	3601	CCTGATTTCTAATATCTAATTTTCTTCAAGAGCTGAGTAATTTGACAGACTCAGAC	3660
QY	3661	GTATGTAAGCTGTAAGATTAATTAATGTTTCTCTTATTAAGAACTTTTCTCTGT	3720
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Db	3721	GGAGTTAGAGCAAGGGCAATCCCGTTTCTTTTAAACAGAGAAACATTCCTTAAG	3780
QY	3781	TAAAGCCAAACGATTCAGAGCTTGAAGTTCCTGACATATATGATTTGGTTTTTGA	3840
Db	3781	TAAAGCCAAACGATTCAGAGCTTGAAGTTCCTGACATATATGATTTGGTTTTTGA	3840
QY	3841	CATTTCAGGAGATGTTACTATCTGATCAGAAAATGAGCTAATCCTTTGGTCACTG	3900
Db	3841	CATTTCAGGAGATGTTACTATCTGATCAGAAAATGAGCTAATCCTTTGGTCACTG	3900
QY	3901	TAAACCAACCCCATTTGTAATGCTCTAAGTTGAGGCTTAATCTGAGAACCAATCAAT	3960
Db	3901	TAAACCAACCCCATTTGTAATGCTCTAAGTTGAGGCTTAATCTGAGAACCAATCAAT	3960

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Db	5040	ATAGGAACATATTATTTGGSGTATGGGTGCATTAANTGGAGTCTTTTAAAAAAGAACT	50939
Qy	5100	CCAAACAGACTTCTGGAAAGTTATTTCTAAGANTCTGTGGCAGCGTGAAGCGAACC	5159
Db	5100	CCAAAGAGCTTTGTGAAGTTATTTCTAAGANTCTGTGGCAGCGTGAAGCGAACC	5159
Qy	5160	CCCTGTGCAGACCCCAACCCAGCTCAAGTGGCACCTCTGTTCGCCCATGAAGAGGCT	5219
Db	5160	CCCTGTGCAGACCCCAACCCAGCTCAAGTGGCACCTCTGTTCGCCCATGAAGAGGCT	5219
Qy	5220	GGCTCCCGCATATATTAACCTCTCTGGAGCTGGGCATGAACGACGAAG	5271
Db	5220	GGCTCCCGCATATATTAACCTCTCTGGAGCTGGGCATGAACGACGAAG	5271

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RESULT 11
AAV51364
ID AAV51364 standard; DNA; 5304 BP.

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AAV51364;

DT 27-OCT-1998 (first entry)

Human TIGR promoter mutant TIGRmt3 DNA.

KM TIGR; trabecular meshwork induced glucocorticoid response protein; human,  
 KM diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.

OS Homo sapiens.

XX  
EH

FT mutation	4997.5002
FT	/*tag= 3

FT /note= "Wild-type TG is replaced with TGTGTG"  
XY

PN	W09832850-A1.
XX	

PD 30-JUL-1998.  
XX

09-JAN-1998; 98MO-US0000468.

PR	28-JAN-1997;	97US-00791154.
PR	26-SEP-1997;	97US-00938669.

XX  
PA (REGC ) UNIV CALIFORNIA.

XX Nguyen TD, Polansky JR, Chen P, Chen H;  
PI

XX  
DR WPI; 1998-427946/36.

PT Use of TIGR nucleic acid sequences - used for, e.g. developing products

XX  
F1 for diagnosis, prognosis and treatment

FS Disclosure; fig 2; 103pp; English.  
XX

CC protein (TIGR) promoter mutant, TIGRmt3, which is used in a method for

polymorphisms whose presence is predictive of a mutation affecting TIG

sensitivity. Base substitutions and base additions upstream of and within

[illegible][illegible]

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Best Local Similarity 99.9%; Pred. No. 0;
Best Global Similarity 99.9%; Pred. No. 0;
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1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

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RESULT 12
AA57485
ID AA57485 standard; DNA; 5304 BP.
XX
AC AA57485;
XX
DT 20-OCT-2000 (first entry)
XX
A TIGR (trabecular meshwork inducible glucocorticoid receptor) promoter.
DE TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;
KW glaucoma; steroid sensitivity; progressive ocular hypertension;
KW vision loss; ss.
XX

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OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH replace(4256, G)  
 FT mutation  
 FT /\*tag= d  
 FT /note= "TIGRmt4 mutant"  
 FT replace(4337, G)  
 FT mutation  
 FT /\*tag= a  
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 FT mutation  
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 FT replace(5117, C)  
 FT /\*tag= e  
 FT /note= "TIGRmt11 mutant"  
 FT mutation  
 FT WO200422220-A1.  
 PD 20-JUL-2000.  
 XX 11-JAN-2000; 2000WO-US000559.  
 XX 11-JAN-1999; 99US-00227681.  
 PR 07-MAY-1999; 99US-00306828.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Nguyen TD, Polansky JR, Chen P, Chen H;  
 PI WPI; 2000-491060/43.  
 DR  
 XX  
 XX  
 PT Diagnosis, prognosis and treatment of glaucoma, based on detecting  
 PT specific polymorphisms in the promoter of the trabecular meshwork  
 PT inducible glucocorticoid receptor gene.  
 XX  
 XX  
 PS Claim 79; Fig 2A-E; 122pp; English.  
 CC The present sequence represents a sequence variant of the TIGR  
 CC (trabecular meshwork inducible glucocorticoid receptor) promoter. The  
 CC specification describes a method for the diagnosis, prognosis and  
 CC treatment of glaucoma, based on detecting specific polymorphisms in the  
 CC promoter of the TIGR gene. The method is used for diagnosis and prognosis  
 CC of glaucoma (of all types), steroid sensitivity and progressive ocular  
 CC hypertension that leads to loss of vision. Glaucoma can be treated by  
 CC administering an agent that binds to cis-acting elements within the TIGR  
 CC promoter. The TIGR promoter (or other regulatory regions) can be used to  
 CC express homologous or heterologous genes, particularly for tissue-  
 CC specific expression of therapeutic transgenes for treating glaucoma, also  
 CC to generate transgenic animals and in screening for compounds (specific  
 CC modulators) with diagnostic or therapeutic potential. Fragments of the  
 CC TIGR sequence can be used as amplification primers or probes, e.g. for  
 CC isolating related sequences in non-human animals  
 XX  
 SQ Sequence 5304 BP; 1481 A; 1150 C; 1239 G; 1434 T; 0 U; 0 Other:  
 Query Match 99.1%; Score 5224.4; DB 3; Length 5304;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 5264; Conservative 0; Mismatches 6; Indels 6; Gaps 3;

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QY 5056 GGGTATGGGTCATAAATTGGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTGG 5115
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 Job time : 1892 secs

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## OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 12:16:22; Search time 12228 Seconds  
(without alignments)  
12872.387 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: em\_hcc:\*  
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19: em\_gss\_pln:\*  
20: em\_gss\_vre:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	186.6	3.5	710	13	BU849843 AGENCOURT
C 2	186.4	3.5	515	14	CA946732 1s09h12.x
C 3	180.8	3.4	660	28	AO057239 CIT-HSP-2
C 4	179.8	3.4	539	28	AO379787 RPII11-15

Result No.	Score	Query Match	Length	ID	Description
C 5	179.2	3.4	340	13	BU957861 AGENCOURT
C 6	179	3.4	597	14	CB268731
C 7	179	3.4	613	28	A2520729 RPII-11-7
C 8	179	3.4	645	28	AO636457 RPII-11-4
C 9	179	3.4	678	28	AO387027 RPII11-15
C 10	178.6	3.4	887	12	BG541228
C 11	178.4	3.4	537	10	AM978041
C 12	177.8	3.4	590	12	BM803650
C 13	177.6	3.4	516	28	AQ112451
C 14	177.4	3.4	577	28	AO265389
C 15	177.2	3.4	548	9	A1583291
C 16	177	3.4	400	10	BF920612
C 17	177	3.4	769	13	BU854207
C 18	176.8	3.4	784	12	BM556091
C 19	176.6	3.4	413	13	EX478124
C 20	176.6	3.4	434	28	AQ159435
C 21	176.6	3.4	573	12	BM990011
C 22	176.6	3.4	591	10	AM979191
C 23	176.4	3.3	501	13	EX646708
C 24	176.4	3.3	568	14	CD517289
C 25	176.2	3.3	494	9	AL698462
C 26	176	3.3	521	10	AM273360
C 27	176	3.3	551	14	TS3829
C 28	175.8	3.3	589	28	AO283440
C 29	175.6	3.3	493	9	AU146498
C 30	175.6	3.3	607	28	B2603705
C 31	175.4	3.3	386	28	AO474222
C 32	175.4	3.3	533	14	CD339747
C 33	175.2	3.3	393	10	BF805088
C 34	175.2	3.3	548	9	AV711892
C 35	175.2	3.3	662	9	AV701462
C 36	175.2	3.3	670	12	BM671184
C 37	175.2	3.3	711	28	AO415030
C 38	175	3.3	388	9	AM699227
C 39	175	3.3	421	10	AM674631
C 40	175	3.3	447	10	AM820784
C 41	175	3.3	454	9	A1634187
C 42	175	3.3	474	9	A1457313
C 43	175	3.3	527	9	A1523813
C 44	175	3.3	546	12	BM697526
C 45	175	3.3	563	9	AU144540

## ALIGNMENTS

RESULT 1  
BU849843/c 710 bp mRNA linear EST 16-OCT-2002

LOCUS AGENCOURT\_10440376 NIH\_MGC\_109 Homo sapiens cDNA clone  
IMAGE:6598537 5', mRNA sequence.

ACCESSION BU849843  
VERSION BU849843.1 GI:24034806

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS 1 (bases 1 to 710)

TITLE: National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov

Plate: LCM2831 row: 1 column: 01  
High quality sequence stop: 592.



The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

[http://www.tigr.org/cdb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html).

Seq primer: M13 Reverse

Class: BAC ends.

#### FEATURES

##### source

Location/Qualifiers  
1. 660  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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/clone="2340D14"  
/sex="Male"  
/cell\_type="Sperm"  
/clone\_lib="CIT-HSP"  
/note="Vector: pBelOAC11, site\_1: HindIII, site\_2: HindIII"

#### ORIGIN

##### Query Match

Best Local Similarity 86.0%; Score 180.8; DB 28; Length 660;

Matches 215; Conservative 0; Mismatches 27; Indels 8; Gaps 1;

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QY 1321 ACCTGAGCTCAGTCAGCACTCTGCTCCCTCCAGTTCAAGCAATTCCTGCTCAGCCTCC 1380
DB 293 ATCTCACTCAGTCAGCACTCTGCTCCCTCCAGTTCAAGCAATTCCTGCTCAGCCTCC 352
QY 1381 CGCGTACCTGGGACTCAGGCG-----CAGCGCCGGCTAATTTTGTATTGTTAGTA 1432
DB 353 CAATGAGCTGGGATTACAGGCGCACACACACAGCCCGGGTAAATTTTGTATTGTTAGTA 412
QY 1433 GAGTGGGGTTTACCATTTAGCCCGGCTGATCTTGAACCTCCTGACCTCAGGTATCCA 1492
DB 413 GAGTGGGGTTTACCATTTAGCCCGGCTGATCTTGAACCTCCTGACCTCAGGTATCCA 472
QY 1493 CCCACCTCAGCCTCTTAAGTGTCTGGATTACAGGCAATGATCAGCCGCCGCCAAG 1552
DB 473 CCCACCTCAGCCTCTTAAGTGTCTGGATTACAGGCAATGATCAGCCGCCGCCAAG 532
QY 1553 GTCACTGTTT 1562
DB 533 TTTTGTATT 542

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#### RESULT 4

LOCUS AQ379787 539 bp DNA linear GSS 20-MAY-1999

DEFINITION RPc11-152C3.TJ RPc1-11 Homo sapiens genomic clone RPc1-11-152C3,

genomic survey sequence.

ACCESSION AQ379787

VERSION AQ379787.1 GI:4350810

#### KEYWORDS

#### SOURCE

#### ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 539)

Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and

#### REFERENCE

#### AUTHORS

#### TITLE

Use of BAC End Sequences from Library RPc1-11 for Sequence-Ready

Map Building

Unpublished (1997)

CONTACT: Shaying Zhao, William Niernan, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hde@tigr.org

Clones are derived from the human BAC library RPc1-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from

Research Genetics (info@resgen.com). BAC end search page:

[http://www.tigr.org/cdb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html)

Seq primer: Sfe

Class: BAC ends.

#### FEATURES

##### source

Location/Qualifiers  
1. 539  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:9606"  
/clone="RPc1-11-152C3"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/clone\_lib="RPc1-11"  
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;  
RPc11 Human Male BAC Library"

#### ORIGIN

##### Query Match

Best Local Similarity 76.8%; Score 179.8; DB 28; Length 539;

Matches 235; Conservative 0; Mismatches 63; Indels 8; Gaps 1;

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QY 1280 AGGTTAGAGGCTCTGTCTTTTACACCTGATGCTCTACACCTGAGCTCAGTCAACC 1339
DB 327 AGAGTCTGCTCTGTACACAGGCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 268
QY 1340 TCTGCTCCCGAGTTCAAGCAATTCCTGCTCAGCCTCCCGAGTCAAGTCAAGTCAAG 1399
DB 267 TCTGCTCCCGAGTTCAAGCAATTCCTGCTCAGCCTCCCGAGTCAAGTCAAGTCAAG 208
QY 1400 GC-----GCACGCCCGGCTAATTTTGTATTGTTAGTAGAGTGGGTTTCAACATA 1451
DB 207 GCATGTGCAACCAATACCCGGCTAATTTTGTATTGTTAGTAGAGTGGGTTTCAACATA 148
QY 1452 TTAGCCCGGCTGCTGTTGAACCTCCTGACCTCAGGTATCACCACCTCAGCCTCTAA 1511
DB 147 TTGACCAAGCTGCTGTTGAACCTCCTGACCTCAGGTATCACCACCTCAGCCTCTAA 88
QY 1512 GTGCTGGATTACAGGCAATGATCAGCCGCCGCCAAGGTCAGTGTATTATAGAA 1571
DB 87 GTGCTGGATTACAGGCAATGATCAGCCGCCGCCAAGGTCAGTGTATTATAGAA 28
QY 1572 TTAATT 1577
DB 27 TGAATT 22

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#### RESULT 5

LOCUS BU957861 340 bp mRNA linear EST 21-OCT-2002

DEFINITION AGENCOURT\_1062879 NIH\_MGC\_141 Homo sapiens cDNA clone

IMAGE:6731972 5', mRNA sequence.

ACCESSION BU957861

VERSION BU957861.1 GI:24187433

#### KEYWORDS

#### SOURCE

#### ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 340)

NIH-MGC <http://mgc.ncl.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: NCI

cDNA Library Preparation: Michael Brownstein Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation



library availability, please contact Pieter de Jong  
(pieterdejong.med.buffalo.edu). Clones may be purchased from  
BACpac Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
Research Genet cs (<http://inforesgen.com>). BAC end search page:  
[http://www.tigr.org/cdb/hungen/bac\\_end\\_search.html](http://www.tigr.org/cdb/hungen/bac_end_search.html).  
This BAC end was generated during the R&D process and may have  
higher chance of clone tracking errors.  
Seq primer: SP6  
Class: BAC ends.

## FEATURES

## Source

## Location/Qualifiers

1. .613  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="GDB:7530100"  
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/clone="RPCT-11-7965"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/clone\_lib="RPCT-11"  
/note="Vector: PBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
RPCT11 Human Male BAC Library"

## ORIGIN

Query Match 3.4%; Score 179; DB 28; Length 613;  
Best Local Similarity 76.4%; Pred. No. 1.4e-25;  
Matches 236; Conservative 0; Mismatches 65; Indels 8; Gaps 1;

1280 AGGCTGAGGCTCTGTCTTACACCTACTGTATGTCTACACCTGAGCTCACTGACACC 1339  
118 AGACTCTTGTCTCTGTGCGCCAGGTGAGTACAGTGTGAGTACAGTCACTGACACC 177  
1340 TCTGCTCCAGGCTTACAGCAATTTCTCTCTTCAAGCTCCGCGTACGTGGACTACAG 1399  
178 TCTGACTCTGTGGTTCAAGCAATTTCTCTCTTCAAGCTCCGCGTACGTGGACTACAG 237  
1400 GCG-----CAGCCCGGCTAATTTTGTATTGTATGATGAGATGGGTTTCAACATA 1451  
238 GTGGCTGCACACAGCTTACTATTTGTATTGTTTGAAGAGATGGGTTTCAACATA 297  
1452 TTAGCCCGGCTGTCTTGAATCTCTGACTCAGGTATCCACCCAGCTCAGCTCTCTTAA 1511  
298 TTGGTCAAGCTGTCTGTGAATCTCTGACTCAGGTATCCACCCAGCTCAGCTCTCTTAA 357  
1512 GTGCTGGATTACAGGCAATGATCAAGCCCGCGGCGCCAGGTTCAAGTATTATTAAGAA 1571  
358 GTGCTGGATTACAGGCGTGAAGCAGCCGCTGTGTTCAAGGCGTGAATGTTTATTAAGAA 417  
1572 TAACTTGA 1580  
418 TAACTTGA 426

RESULT 8  
AO636457/c

LOCUS 645 bp DNA linear GSS 17-JUN-1999  
DEFINITION RPCT-11-465121.TV RPCT-11 Homo sapiens genomic clone  
ACCESSION AO636457  
VERSION AO636457.1 GI:5099092  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 645)  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and  
Venter,J.C.  
Use of BAC End Sequences from Library RPCT-11 for Sequence-Ready  
Map Building  
Unpublished (1997)

## JOURNAL

COMMENT  
Contact: Shaying Zhao, William Niernan, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are derived from the human BAC library RPCT-11. For BAC  
library availability, please contact Pieter de Jong  
(pieterdejong.med.buffalo.edu). Clones may be purchased from  
BACpac Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
Research Genet cs (<http://inforesgen.com>). BAC end search page:  
[http://www.tigr.org/cdb/hungen/bac\\_end\\_search.html](http://www.tigr.org/cdb/hungen/bac_end_search.html).  
Seq primer: SP6  
Class: BAC ends.

## FEATURES

## Source

## Location/Qualifiers

1. .645  
/organism="Homo sapiens"  
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/db\_xref="GDB:767838"  
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/clone="RPCT-11-465121"  
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/note="Vector: PBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
RPCT11 Human Male BAC Library"

## ORIGIN

Query Match 3.4%; Score 179; DB 28; Length 645;  
Best Local Similarity 88.2%; Pred. No. 1.4e-25;  
Matches 209; Conservative 0; Mismatches 20; Indels 8; Gaps 1;

1322 CTTGAGTCACTGCAACTCTGCTCCAGTTCAAGCAATTTCTCTGCTCAGGCTCCC 1381  
248 CTTGAGTCACTGCAACTCTGCTCCAGTTCAAGCAATTTCTCTGCTCAGGCTCCC 189  
1382 GCGTACGTGGACTACAGCG-----CAGCCCGGCTAATTTTGTATTGTTAGTNG 1433  
188 GAGTACGTGGATTACAGGCGGTGTATCAACAGCCAGCTAATTTTGTATTGTTAGTNG 129  
1434 AGATGGGTTTACACATATTAGCCCGGCTGTGTTTAACTCTGAGCTGATGCCAC 1493  
128 AGATGGGATTTCACATATTGTCAGAGCTGTCTCCGACTCTGAGCTCAAGTATGCTGC 69  
1494 CCACCTCAGGCTCTTAAGTGTGGATTACAGGCAATGATCAACCGCGCGGCCA 1550  
68 CCACCTCAGGCTCTTAAGTGTGGATTACAGGCAATGATGATGATGATGATGATGATGAT 12

RESULT 9  
AO387027/c

LOCUS 678 bp DNA linear GSS 21-MAY-1999  
DEFINITION RPCT11-153C12.TV RPCT-11 Homo sapiens genomic clone RPCT-11-153C12,  
genomic survey sequence.  
ACCESSION AO387027  
VERSION AO387027.1 GI:4358050  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 678)  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and  
Venter,J.C.  
Use of BAC End Sequences from Library RPCT-11 for Sequence-Ready  
Map Building  
Unpublished (1997)

## JOURNAL

COMMENT  
Contact: Shaying Zhao, William Niernan, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org





Email: johnq@tigr.org  
Plate: 387  
Seq primer: Forward.  
Location/Qualifiers  
1. 537  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE ressequences, YAGO"  
/note="Vector: pBluescriptSKm"

## ORIGIN

Query Match 3.4%; Score 178.4; DB 10; Length 537;  
Best Local Similarity 77.2%; Pred. No. 1.8e-25;  
Matches 233; Conservative 0; Mismatches 61; Indels 8; Gaps 1;

OY 1281 GGGTGAAGGCTCTGTCTTCTTACCTACCTGATGCTCTACCTGAGCTCACTGCAACT 1340  
DB 6 GAGTCTGTCTGTCTGTCCAGAGCTGAGTGCATGATGCTCGGCTCACTGCAAACT 65  
OY 1341 CTGGCTCCAGGTTCAAGCAATTCCTCTCTCAAGCTCCCGGTAGCTGGGACTACAG 1400  
DB 66 CCACTCCCAAGTTCAAGCAATTCCTCTCTCAAGCTCCCGGTAGCTGGGACTACAG 125  
OY 1401 CG-----CAGCCCGGCTAATTTTGTATTGTATAGATAGAGATGGGGTTTCAACCAT 1452  
DB 126 TGCCCAACACCAACCAACCACTAATTTTGTATTGTATAGATAGAGATGGGGTTTCAACCAT 185  
OY 1453 TAGCCCGGCTGTCTTGAACCTCTGACCTCAGGTATCCACCACTCAGCTCTTAAG 1512  
DB 186 TGCCAGACTGTCTCCAGCTCTGACCTCAGGTATCCACCACTCAGCTCTTAAG 245  
OY 1513 TGCTGGATTATAGAGCTGAGTACCGCGCCGCAAGGAGTGTATTAAGGAAT 1572  
DB 246 TGCTGGATTATAGAGCTGAGTACCGCGCCGCAAGGAGTGTATTAAGGAAG 305  
OY 1573 AA 1574  
DB 306 AA 307

RESULT 12  
BM803650 990 bp mRNA linear EST 05-MAR-2002  
LOCUS  
AGENCOURT 6439541 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:5520297  
DEFINITION  
5' mRNA sequence.

ACCESSION  
BM803650  
VERSION  
BM803650.1 GI:19120473  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 990)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM12184 row: b column: 10  
High quality sequence stop: 632.  
Location/Qualifiers  
1. 990  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"

## FEATURES

source

/clone="IMAGE:5520297"  
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/lab\_host="PH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_71"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 2.1 kb."

## ORIGIN

Query Match 3.4%; Score 177.8; DB 12; Length 990;  
Best Local Similarity 82.9%; Pred. No. 2.3e-25;  
Matches 218; Conservative 0; Mismatches 37; Indels 8; Gaps 1;

OY 1327 GCTCACTGCAACTCTGCTCCAGGTTCAAGCAATTCCTCTCTCAAGCTCCCGGTA 1386  
DB 97 GCTTACTGCAACTCCCACTCCAGGATCAATGATTCCTCTCTCAAGCTCCCGGTA 156  
OY 1387 GCTGGAGCTACAGCG-----CAGCCCGGCTAATTTTGTATTGTAGTAGAGATG 1438  
DB 157 GCTGGAGTACAGCGCCCGCCCAACATGCAAGGCTAATTTTGTATTGTAGTAGAGAG 216  
OY 1439 GGGTTTCAACATATTAGCCCGGCTGCTTGAATCTGACCTCAGTGATCAACCAAC 1498  
DB 217 AGGTTTCAACATATTGAGCCAGGCTGCTGAACTCTGACCTCAGTGATCAACCAAC 276  
OY 1499 TCAAGCTCTTAAAGTCTGGGATTACAGGATGATGATGATGATGATGATGATGAT 1558  
DB 277 TCGGCTCTTAAAGTCTGGGATTACAGGATGATGATGATGATGATGATGATGAT 336  
OY 1559 GTTAAATAGGATTAATTAAT 1581  
DB 337 AATTTTAAAGAAATCTTCAAT 359

## RESULT 13

LOCUS  
A0112451 516 bp DNA linear GSS 29-AUG-1998  
DEFINITION  
CIT-HSP-2372C9.TF CIT-HSP Homo sapiens genomic clone 2372C9,  
genomic survey sequence.

ACCESSION  
A0112451  
VERSION  
A0112451.1 GI:3484611  
KEYWORDS  
GSS.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 516)  
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and  
Venter,J.C.  
Use of a random human BAC End Sequence Database for Sequence-Ready  
Map Building  
Unpublished (1998)  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: madams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/tbdb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13-21  
Class: BAC ends.

TITLE  
JOURNAL  
COMMENT  
Map Building  
Unpublished (1998)  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: madams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/tbdb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13-21  
Class: BAC ends.

## FEATURES

source

1. 516  
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/sex="Male"

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 /clone\_lib="CIT-HSP"  
 /note="Vector: pBelobAC11, site\_1: HindIII; site\_2: HindIII"

Query Match 3.4%; Score 177.6; DB 28; Length 516;  
 Best Local Similarity 85.2%; Pred. No. 2.7e-25;  
 Matches 213; Conservative 0; Mismatches 29; Indels 8; Gaps 1;

QY 1321 ACCGAGCTCAGCGAAGCCCTCCGAGGTTCAAGAAATTCCTGTCAGACCTCC 1380  
 DB 255 ATCTCAGCTCAGCGAAGCCCTCCGAGGTTCAAGAAATTCCTGTCAGACCTCC 314  
 QY 1381 CGCGTAGCTGGAGCTACAGCGC-----CAGCGCCGCGCTAATTTTGTATTGTA 1432  
 DB 315 CAGTAGCTGGAGCTACAGCGCAGCAGCAGCGCGCTAATTTTGTATTGTA 374  
 QY 1433 GAGATGGGCTTACCAATATTAAGCCGCGTGTCTTGAATCTGACCTCAGGTATCA 1492  
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 VERSION AO265389.1 GI:3793589  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
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 1 (bases 1 to 577)  
 Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
 Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and  
 Venter,J.C.  
 Use of a random human BAC End Sequence Database for Sequence-Ready  
 Map Building  
 Unpublished (1998)  
 Other GSSs: CITBI-EI-2509010.TR  
 Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: mdadams@tigr.org  
 Clones are available from Research Genetics (info@resgen.com). BAC  
 end search page:  
 http://www.tigr.org/tdb/hungen/bac\_end\_search/bac\_end\_search.html.  
 Seg primer: M13-21  
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Caltech Human BAC Library D"

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 Best Local Similarity 75.1%; Pred. No. 2.9e-25;  
 Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;

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 DB 308 CAGTAGCTGGAGCTACAGCGCAGCAGCAGCGCTAATTTTGTATTGTA 249  
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 DB 248 GAGATGGGCTTACCAATATTAAGCCGCGTGTCTTGAATCTGACCTCAGGTATCA 189  
 QY 1493 CCCACCTCAGCTCTTAAAGTGTGGATTACAGCATAGTACCGCGCCGCGCAAG 1552  
 DB 188 CCCACCTGCGCTCCCAAGTGTGGATTACAGCATAGTACCGCGCCAGCTAAT 129  
 QY 1553 GTCAAGTCTTAAATGAATAGTGAATGTTTACTTAAACCAAGGAAACAGACAA 1612  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 548)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgsrps-remail.nih.gov  
 Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,  
 M.D., Ph.D.  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the T.M.A.G.E. Consortium/LINL at:  
 www.bio.lnlnl.gov/bdrp/image/image.html  
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/note="Organ: bone marrow; Vector: PAMPI; mRNA made from lymphoid tissue, cDNA made by oligo-dt priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

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Query Match      3.4%; Score 177.2; DB 9; Length 548;
Best Local Similarity 78.8%; Pred. No. 3.2e-25;
Matches 227; Conservative 0; Mismatches 53; Indels 8; Gaps 1;

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QY 1337 ACCTCTGCTCCAGGCTTCAAGCAATTCTCTGTCTCAGCTCCGCGTACTGAGACTA 1396
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DB 486 ACCTCCGCTCAGAGGTTCAAGCAATTCTCTGCTCAGCTCCGCGTACTGAGACTA 427
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QY 1509 AAAGTCTGGGATTAAGAGCATGAGTACCGGCGCGGCGCAAGGTCA 1556
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DB 306 AAAGTCTGGGATTAAGAGCATGAGTACCGGCGCGGCGCAAGGTCA 259
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 12:16:22 ; Search time 2222 Seconds  
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11973.488 Million cell updates/sec

Title: US-09-227-881-34

Perfect score: 5271

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Scoring table:

IDENTITY NUC  
Gapop 10.0 , Gapept 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:\*  
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and is derived by analysis of the total score distribution.

## SUMMARIES

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C 25	180.6	3.4	66933	16	US-10-374-979-11	Sequence 11, Appl
C 26	180.6	3.4	66933	17	US-10-731-739-11	Sequence 9, Appl
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## ALIGNMENTS

## RESULT 1

US-10-244-633-34

Sequence 34, Application US//10244633

Publication No. US20030068640A1

GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.

APPLICANT: Polansky, Jon R.

APPLICANT: Chen, Hu

TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,

TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related

TITLE OF INVENTION: Disorders

FILE REFERENCE: 07425.0057.0501

CURRENT APPLICATION NUMBER: US/10/244, 633

CURRENT FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: US/09/306, 828

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: US 09/227, 861

PRIOR FILING DATE: 1999-01-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Microsoft Word 97

SEQ ID NO 34

LENGTH: 5271

TYPE: DNA

ORGANISM: Homo sapiens

US-10-244-633-34

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2401 CCAGAAAGGAAATGAGAGAGGAAATCTAGTCTAAACGAGAAATCTGAGAGGAGAGAGTTTTC 2460  
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Qy 2641 CTTTATCTTTTCTCTGCTTGAGAGAGAGAGTCTATTCATGAGAGGATGCAATTTC 2700  
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Qy 2701 ATAAAGTCAAGTGTAAATTCAG3GTGCAATGG3TTTCTCTTCAAGAGCCTTAT 2760  
Db ATAAAGTCAAGTGTAAATTCAG3GTGCAATGG3TTTCTCTTCAAGAGCCTTAT 2760  
Qy 2761 TTAATGGAAATATGAGAGGAGCTATTCCTAGGCGCTTAATTCACG3AAGAGTAC 2820  
Db TTAATGGAAATATGAGAGGAGCTATTCCTAGGCGCTTAATTCACG3AAGAGTAC 2820  
Qy 2821 TGAAGTCTTTTCTTCAATGTCTTCTG3GCAATCACTCAAGCCTGTG3TGAATGCACTT 2880  
Db TGAAGTCTTTTCTTCAATGTCTTCTG3GCAATCACTCAAGCCTGTG3TGAATGCACTT 2880  
Qy 2881 TGCAGAGCGTGCAGAAACCTTGAATCAGAGAGCTGG3TTTCTCTG3TTCGATTC 2940  
Db TGCAGAGCGTGCAGAAACCTTGAATCAGAGAGCTGG3TTTCTCTG3TTCGATTC 2940  
Qy 2941 GGTGCTGTGCGACG3TGG3CAAGTGTCTCTCTTCCCTG3GCAATGCTTCTGCT 3000  
Db GGTGCTGTGCGACG3TGG3CAAGTGTCTCTCTTCCCTG3GCAATGCTTCTGCT 3000  
Qy 3001 ATAAAGACCTTTCAGCTCTGTGTCTGTGAACATTCCTCTGTGATCTCTGTGAG3G3 3060  
Db ATAAAGACCTTTCAGCTCTGTGTCTGTGAACATTCCTCTGTGATCTCTGTGAG3G3 3060  
Qy 3061 GATGTGTGAGAGG3AAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120  
Db GATGTGTGAGAGG3AAG 3120  
Qy 3121 G3ACAG 3180  
Db G3ACAG 3180  
Qy 3181 CAGAGCGAG 3240  
Db CAGAGCGAG 3240  
Qy 3241 TCCCTAAGCATAGACATGAGCATTTGCCAATTAACAAAGAGAGAGAGAGAGAGAG 3300  
Db TCCCTAAGCATAGACATGAGCATTTGCCAATTAACAAAGAGAGAGAGAGAGAGAG 3300  
Qy 3301 G3TACCTTTTGGCTG3CATTCAGAAACCTGG3GAGAGAGAGAGAGAGAGAGAGAG 3360  
Db G3TACCTTTTGGCTG3CATTCAGAAACCTGG3GAGAGAGAGAGAGAGAGAGAGAG 3360  
Qy 3361 TTAACCTTTTACCGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420  
Db TTAACCTTTTACCGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420  
Qy 3421 AGTACCTGCAGCGAG 3480  
Db AGTACCTGCAGCGAG 3480  
Qy 3481 ACAGATTCATTCAG 3540  
Db ACAGATTCATTCAG 3540  
Qy 3541 GTTCTAG 3600  
Db GTTCTAG 3600  
Qy 3601 CCGATTTCTTAATCAATATTTTCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 3660  
Db CCGATTTCTTAATCAATATTTTCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 3660  
Qy 3661 GTAGTACAG 3720  
Db GTAGTACAG 3720  
Qy 3721 G3AGTTAG 3780  
Db G3AGTTAG 3780  
Qy 3781 TTAAGCCAAACAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3840  
Db TTAAGCCAAACAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3840  
Qy 3841 CATTGACAGATTTTCAATCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900  
Db CATTGACAGATTTTCAATCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900  
Qy 3901 TTAACCAACAG 3960  
Db TTAACCAACAG 3960  
Qy 3961 AGATAGAGATTTTAG 4020  
Db AGATAGAGATTTTAG 4020  
Qy 4021 AGTTGGAATTTTACTTCAAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4080  
Db AGTTGGAATTTTACTTCAAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4080  
Qy 4081 TGCCTAAG 4140  
Db TGCCTAAG 4140  
Qy 4141 TTATGCTATTTGCAATTTGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 4200  
Db TTATGCTATTTGCAATTTGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 4200  
Qy 4201 G3ATTTATTAACCTTCAAG 4260  
Db G3ATTTATTAACCTTCAAG 4260  
Qy 4261 TGTTTTACAG 4320  
Db TGTTTTACAG 4320  
Qy 4321 CTCAAG 4380  
Db CTCAAG 4380  
Qy 4381 TTAATCAATTAATCAAG 4440  
Db TTAATCAATTAATCAAG 4440  
Qy 4441 CTTGAAATTAAG 4500  
Db CTTGAAATTAAG 4500

Db 4441 CTTGAATATGAGACTCTGCTGATCTTTTACATATTAATAAAGATTTTAA 4500  
QY 4501 ATTTGATATTTGATTAATCATATTCATATTCATTTGCTTGAATCATATTTT 4560  
Db 4501 ATTTGATATTTGATTAATCATATTCATATTCATTTGCTTGAATCATATTTT 4560  
QY 4561 ATATATTTGAAAACATCTTTCTGAGAGAGTCCCAAGATTTACCAATGAGTTCTTG 4620  
Db 4561 ATATATTTGAAAACATCTTTCTGAGAGAGTCCCAAGATTTACCAATGAGTTCTTG 4620  
QY 4621 CATGACACACACAGAGTAAAGATTTAGAGTAAATGATGATGATGATGATGATG 4680  
Db 4621 CATGACACACACAGAGTAAAGATTTAGAGTAAATGATGATGATGATGATGATG 4680  
QY 4681 TGCAGAGCTGAATTTGAAAGTCTCCCAAGATTTACCAATGAGTTCTTG 4740  
Db 4681 TGCAGAGCTGAATTTGAAAGTCTCCCAAGATTTACCAATGAGTTCTTG 4740  
QY 4741 AGGGGGGAAATCTGCGCTTTCTATAGAGATGCTTCTCCGAGCTGAGGCTGAGGCTG 4800  
Db 4741 AGGGGGGAAATCTGCGCTTTCTATAGAGATGCTTCTCCGAGCTGAGGCTGAGGCTG 4800  
QY 4801 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4860  
Db 4801 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4860  
QY 4861 GATCTTCCAGTCTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4920  
Db 4861 GATCTTCCAGTCTTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4920  
QY 4921 TGAATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4980  
Db 4921 TGAATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4980  
QY 4981 TGAATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5040  
Db 4981 TGAATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5040  
QY 5041 TAGGAATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5100  
Db 5041 TAGGAATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5100  
QY 5101 CAACAGACTTCTGAGAGTATTTCTTAAGATTTCTGAGAGCTGAGAGCTGAGAGCTG 5160  
Db 5101 CAACAGACTTCTGAGAGTATTTCTTAAGATTTCTGAGAGCTGAGAGCTGAGAGCTG 5160  
QY 5161 CCGTGTGACAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTG 5220  
Db 5161 CCGTGTGACAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTG 5220  
QY 5221 GCTCCCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5271  
Db 5221 GCTCCCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5271

RESULT 2  
US-10-244-633-3  
; Sequence 3, Application US/10244633  
; Publication No. US20030068640A1  
; GENERAL INFORMATION:  
; APPLICANT: Nguyen, Thai D.  
; APPLICANT: Polansky, Jon R.  
; APPLICANT: Chen, Pu  
; APPLICANT: Chen, Hua  
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,  
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related  
; TITLE OF INVENTION: Disorders  
; FILE REFERENCE: 07425, 0057, US01  
; CURRENT APPLICATION NUMBER: US/10/244, 633  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: US/09/306, 828  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: US 09/227, 881

; PRIOR FILING DATE: 1999-01-11  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Microsoft Word 97  
; SEQ ID NO 3  
; LENGTH: 6169  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-244-633-3

Query Match 100.0%; Score 5271; DB 15; Length 6169;  
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;  
Matches 5271; Conservative 0; Mismatches 0

QY 1 ATCTTTGCTCACTTACCTGAGGCTATTAAGAAATGAAATGAAATGAAATGAAATGAAATG 60  
Db 1 ATCTTTGCTCACTTACCTGAGGCTATTAAGAAATGAAATGAAATGAAATGAAATGAAATG 60  
QY 61 TCCCTTAATGCTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
Db 61 TCCCTTAATGCTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
QY 121 GGAAGAGAGATATCCAGTTAGCCAGTGTCCAGGCTGTGTGCTCTTATTTAGTGA 180  
Db 121 GGAAGAGAGATATCCAGTTAGCCAGTGTCCAGGCTGTGTGCTCTTATTTAGTGA 180  
QY 181 CAGATGTTGCTCTGACAGAACTTATTTAGAGAAATCATCATCATCATCATCATCATCAT 240  
Db 181 CAGATGTTGCTCTGACAGAACTTATTTAGAGAAATCATCATCATCATCATCATCATCAT 240  
QY 241 CATCAACAGAGAGCTTAAGAAACAGAAATGAGATGAGATGAGATGAGATGAGATGAGATG 300  
Db 241 CATCAACAGAGAGCTTAAGAAACAGAAATGAGATGAGATGAGATGAGATGAGATGAGATG 300  
QY 301 GAGAGCAATTAATGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360  
Db 301 GAGAGCAATTAATGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360  
QY 361 ATGAGAGCAATTAATGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420  
Db 361 ATGAGAGCAATTAATGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420  
QY 421 TAATTAATTAATTTGCTGCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Db 421 TAATTAATTAATTTGCTGCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
QY 481 AAAGCTCAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
Db 481 AAAGCTCAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
QY 541 GGCATCACTCTGAGGAGGCAAGTTCAGGAAAGTTCATGTAAGAGAGAGAGAGAGAGAGAG 600  
Db 541 GGCATCACTCTGAGGAGGCAAGTTCAGGAAAGTTCATGTAAGAGAGAGAGAGAGAGAGAG 600  
QY 601 AGCAAAATCAAAATTTCCGCAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
Db 601 AGCAAAATCAAAATTTCCGCAAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
QY 661 AGTATTAAGAGAGTGAACATGTTGCAACACCTCCCGCTCTATACAGAGAGAGAGAGAG 720  
Db 661 AGTATTAAGAGAGTGAACATGTTGCAACACCTCCCGCTCTATACAGAGAGAGAGAGAG 720  
QY 721 ATTAGCTGGCTTAAGCTGAGCTTTCAAGGGAATTAAGAAATTAAGAGAGAGAGAGAG 780  
Db 721 ATTAGCTGGCTTAAGCTGAGCTTTCAAGGGAATTAAGAAATTAAGAGAGAGAGAGAG 780  
QY 781 GACATGTTAAAG 840  
Db 781 GACATGTTAAAG 840  
QY 841 GGGAGCCCTGAG 900  
Db 841 GGGAGCCCTGAG 900

Qy	901	TTGAAAGATCATGTTTTTAAACATTTTAAATGAAATATGCGATGCAATATG	960
Db	901	TTGAAAGATCATGTTTTTAAACATTTTAAATGAAATATGCGATGCAATATG	960
Qy	961	TTTGAAGATCGGTCCTCAATTTTAAAGTCAGGCATACAAAGTAACTGTGCCAGCTCC	1020
Db	961	TTTGAAGATCGGTCCTCAATTTTAAAGTCAGGCATACAAAGTAACTGTGCCAGCTCC	1020
Qy	1021	GGATAGGTGCAAAATCATTTGAAATCACTGTGTCCCATCTTACTTTTTCAGATGATC	1080
Db	1021	GGATAGGTGCAAAATCATTTGAAATCACTGTGTCCCATCTTACTTTTTCAGATGATC	1080
Qy	1081	TGTATAGCCCTCACAACAAGGCCCATGTGTCTGACCTAACACACATCTCAACCCAA	1140
Db	1081	TGTATAGCCCTCACAACAAGGCCCATGTGTCTGACCTAACACACATCTCAACCCAA	1140
Qy	1141	GTGCTTCAACCATTTGTTAACTGTCTCATAGAGTCCCATTAACAAATGCCACCTCCCC	1200
Db	1141	GTGCTTCAACCATTTGTTAACTGTCTCATAGAGTCCCATTAACAAATGCCACCTCCCC	1200
Qy	1201	TGTGACGCCATCCCGCTCAACAAGAGTCCCACTCTAGACTTCTGACATCAAGATG	1260
Db	1201	TGTGACGCCATCCCGCTCAACAAGAGTCCCACTCTAGACTTCTGACATCAAGATG	1260
Qy	1261	TACAGCCAGAAGCTCCGTGAGGGTGAAGGATGTGTCTTACACTTACCTGATGTCTTAC	1320
Db	1261	TACAGCCAGAAGCTCCGTGAGGGTGAAGGATGTGTCTTACACTTACCTGATGTCTTAC	1320
Qy	1321	ACCTGAGCTACTGTCACAACTCTGTCTCCCAAGTTCAAGCAATCTCTGTCTCAAGCTCC	1380
Db	1321	ACCTGAGCTACTGTCACAACTCTGTCTCCCAAGTTCAAGCAATCTCTGTCTCAAGCTCC	1380
Qy	1381	CGCGTAGCTGGGACTACAGCGCGCACGCCCGCTAATTTTGTATGTTAGTAGAGATGGG	1440
Db	1381	CGCGTAGCTGGGACTACAGCGCGCACGCCCGCTAATTTTGTATGTTAGTAGAGATGGG	1440
Qy	1441	GTTTCACCATTTAGCCCGGTGTCTTGAATCTTGAACCTCAAGTGAATCCACCACTTC	1500
Db	1441	GTTTCACCATTTAGCCCGGTGTCTTGAATCTTGAACCTCAAGTGAATCCACCACTTC	1500
Qy	1501	AGCCTCTAAAGTCTGGGATTAACAGGCATGAGTCAACCGGCCCGGCAAGAGTCAAGT	1560
Db	1501	AGCCTCTAAAGTCTGGGATTAACAGGCATGAGTCAACCGGCCCGGCAAGAGTCAAGT	1560
Qy	1561	TTAATTAAGGAATTAATGATGTTTCTTAACCAACAAGGAAACAGATAAAGCTGTGA	1620
Db	1561	TTAATTAAGGAATTAATGATGTTTCTTAACCAACAAGGAAACAGATAAAGCTGTGA	1620
Qy	1621	TAAATTAAGGAATTAATGATGTTTCTTAACCAACAAGGAAACAGATAAAGCTGTGA	1680
Db	1621	TAAATTAAGGAATTAATGATGTTTCTTAACCAACAAGGAAACAGATAAAGCTGTGA	1680
Qy	1681	CACTGTCCTCATCACTTCTTCCCTCATCTCATATTTTCAGGCTAAGTTACATTTAT	1740
Db	1681	CACTGTCCTCATCACTTCTTCCCTCATCTCATATTTTCAGGCTAAGTTACATTTAT	1740
Qy	1741	CACCATGCTTTTGTGTGTAAGCTTCCACATGTTTACGAAATAGAGTATACATAAATG	1800
Db	1741	CACCATGCTTTTGTGTGTAAGCTTCCACATGTTTACGAAATAGAGTATACATAAATG	1800
Qy	1801	TTTCATTTGGGGCATCTGTGTGTATAGGGGAGAGGACATACCCCAAGACTCCT	1860
Db	1801	TTTCATTTGGGGCATCTGTGTGTATAGGGGAGAGGACATACCCCAAGACTCCT	1860
Qy	1861	TGAAGCCCCCGCAGAGGTTTCTCTCAAGCTGGGGAGCCCTGCAAGAACCCCGGGTCC	1920
Db	1861	TGAAGCCCCCGCAGAGGTTTCTCTCAAGCTGGGGAGCCCTGCAAGAACCCCGGGTCC	1920
Qy	1921	TGGGTGCTTGAAGCACTGCAAGCCGTGCACTGTGTGTGTATATCACTCTTAGG	1980
Db	1921	TGGGTGCTTGAAGCACTGCAAGCCGTGCACTGTGTGTGTATATCACTCTTAGG	1980
Qy	1981	GACCTGTGCTTTCTAATTTCTGTGTGACGTGTCATTCATCAAGGCATTCATGACAT	2040
Db	1981	GACCTGTGCTTTCTAATTTCTGTGTGACGTGTCATTCATCAAGGCATTCATGACAT	2040
Qy	2041	TATTAAGTACTTATATCTGCGACACACAGACAAATGTGTAGCAAAAGCATCTAC	2100
Db	2041	TATTAAGTACTTATATCTGCGACACACAGACAAATGTGTAGCAAAAGCATCTAC	2100
Qy	2101	CCATCCTGTGAGGATGACATTTCTCATGGAACAGTGCAGAAAGAAATTAATAGCA	2160
Db	2101	CCATCCTGTGAGGATGACATTTCTCATGGAACAGTGCAGAAAGAAATTAATAGCA	2160
Qy	2161	GCCAACTTAAACCACTGTGTAAGAAAGAAATTAACACATCTTGAGATTTGTGCG	2220
Db	2161	GCCAACTTAAACCACTGTGTAAGAAAGAAATTAACACATCTTGAGATTTGTGCG	2220
Qy	2221	AGCATCCCTTAACAAGCCACCTCCCTAGCGCCCGCTGCTGCATCTGTGCCGAGG	2280
Db	2221	AGCATCCCTTAACAAGCCACCTCCCTAGCGCCCGCTGCTGCATCTGTGCCGAGG	2280
Qy	2281	CCCCCAAGCCGAGTCTTCAAGACCTCTCTCATAGTACACAGCGCTGACGTGCT	2340
Db	2281	CCCCCAAGCCGAGTCTTCAAGACCTCTCTCATAGTACACAGCGCTGACGTGCT	2340
Qy	2341	GCTTCCGTTCCGTGAATGTCTGTGTGATTTGATGCTGAGACCTCTTGTGCTCAAGCT	2400
Db	2341	GCTTCCGTTCCGTGAATGTCTGTGTGATTTGATGCTGAGACCTCTTGTGCTCAAGCT	2400
Qy	2401	CCAGAAAGGAATGAGAGGAGAACTAGTCTAACAGAGATCTGAGGGGACAGTGTTC	2460
Db	2401	CCAGAAAGGAATGAGAGGAGAACTAGTCTAACAGAGATCTGAGGGGACAGTGTTC	2460
Qy	2461	CTCAGAGGAGAGGAGGCTTCCAGTCCAGAGAGATTTCAAGAGTGGGACTGCAAGGAG	2520
Db	2461	CTCAGAGGAGAGGAGGCTTCCAGTCCAGAGAGATTTCAAGAGTGGGACTGCAAGGAG	2520
Qy	2521	TGGGAGACGCTGGGGCTGAGACGGGTGTGTAAGGACAGAAAGTGAAGAGGCAAGCTAA	2580
Db	2521	TGGGAGACGCTGGGGCTGAGACGGGTGTGTAAGGACAGAAAGTGAAGAGGCAAGCTAA	2580
Qy	2581	GCTGCCAGATGTTTCACTGTTGTCAACGGAGCTGGAGATTTCCGTTCTTCCGTGAGC	2640
Db	2581	GCTGCCAGATGTTTCACTGTTGTCAACGGAGCTGGAGATTTCCGTTCTTCCGTGAGC	2640
Qy	2641	CTTTTATCTTTTCTCTGCTTGAAGAGAAAGTCTATTTCAATGAAGGATGCAATTC	2700
Db	2641	CTTTTATCTTTTCTCTGCTTGAAGAGAAAGTCTATTTCAATGAAGGATGCAATTC	2700
Qy	2701	ATAAGTACGCTTTAAATTCAGAGGTGTGATGAGTTTCTTCAAGAAAGCTTTAT	2760
Db	2701	ATAAGTACGCTTTAAATTCAGAGGTGTGATGAGTTTCTTCAAGAAAGCTTTAT	2760
Qy	2761	TTAATGGAATATAGGAAGGACATCTTCTAGCCGTTAATTCACAGAAAGTATAC	2820
Db	2761	TTAATGGAATATAGGAAGGACATCTTCTAGCCGTTAATTCACAGAAAGTATAC	2820
Qy	2821	TGAAGTCTTTCTTATGATGCTTCTGAGCAATACCTCAAGCCCTGTGTGAGCTTGA	2880
Db			

Db 3061 GGAATTGAGAGGGGAAAGAGGCGAGCTGAGACAGCTGAGCCACAGGGGAGGTGAGGG 3120  
Qy 3121 GGAAGAGAGGAGGAGAGAGGTGGGTGCTCCATGATCTCATGATCAAGTCAGATC 3180  
Db 3121 GGAAGAGAGGAGGAGAGAGGTGGGTGCTCCATGATCTCATGATCAAGTCAGATC 3180  
Qy 3181 CAGAGCCGAGAGGAGAGAGGCTTCAGAGAAAGCTGAATGAAACCAACAGCAATTTTCT 3240  
Db 3181 CAGAGCCGAGAGGAGAGAGGCTTCAGAGAAAGCTGAATGAAACCAACAGCAATTTTCT 3240  
Qy 3241 TCCCTAAGCATAGACATGAGCATTTGCGCAATACCAAAAAGATGACAGATCACTGGT 3300  
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Qy 3301 GGTAGCTTTTGGCTGGCATTTCAAAAAGTGGCCAGAGCAAGTGGCAAAATGCGCAGAGTTG 3360  
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Qy 3361 TTTAACTTTTCACTGACAGACAGCCAGAGCTCAGCAGTGACTGTCAGACAGCAG 3420  
Db 3361 TTTAACTTTTCACTGACAGACAGCCAGAGCTCAGCAGTGACTGTCAGACAGCAG 3420  
Qy 3421 AGTGAAGCTGAGCGCAGAGGAGAGAGAGAGAGAGAGAGAGATGTATAGAGAGAGAG 3480  
Db 3421 AGTGAAGCTGAGCGCAGAGGAGAGAGAGAGAGAGAGAGAGATGTATAGAGAGAGAG 3480  
Qy 3481 ACAGATTCATTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540  
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Qy 3541 GTTCTAG 3600  
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Qy 3661 GTAGTACTGAGAGCTGTAAGATTACTTACTTACTTACTTACTTACTTACTTACTTACTT 3720  
Db 3661 GTAGTACTGAGAGCTGTAAGATTACTTACTTACTTACTTACTTACTTACTTACTTACTT 3720  
Qy 3721 GGAATTCAG 3780  
Db 3721 GGAATTCAG 3780  
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Db 3781 TAAAGCCAAACAGATTCAG 3840  
Qy 3841 CATTCAG 3900  
Db 3841 CATTCAG 3900  
Qy 3901 TAAACAAACAG 3960  
Db 3901 TAAACAAACAG 3960  
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Db 4021 AGTTTGGAAATATTTTCTTCAAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4080  
Qy 4081 TGGTCAAG 4140  
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Qy 4141 TTAATGGCTATTCAG 4200  
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Qy 4201 GGATTAATTAACCTACAGTCAG 4260  
Db 4201 GGATTAATTAACCTACAGTCAG 4260  
Qy 4261 TGTATTTTACAGCTTCTACATTAATTTTACATTTTACATTTTACATTTTACATTTTACAT 4320  
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Qy 4321 CTCAAGGTGATTAACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 4380  
Db 4321 CTCAAGGTGATTAACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 4380  
Qy 4381 TTAATCTAATTAACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 4440  
Db 4381 TTAATCTAATTAACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 4440  
Qy 4441 CTTGAAATTAAGAGCTTCTGAG 4500  
Db 4441 CTTGAAATTAAGAGCTTCTGAG 4500  
Qy 4501 ATTTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 4560  
Db 4501 ATTTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 4560  
Qy 4561 ATTTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 4620  
Db 4561 ATTTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 4620  
Qy 4621 ATTTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 4680  
Db 4621 ATTTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 4680  
Qy 4681 ATTTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 4740  
Db 4681 ATTTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 4740  
Qy 4741 AGGAGGAG 4800  
Db 4741 AGGAGGAG 4800  
Qy 4801 CTTGATTCAG 4860  
Db 4801 CTTGATTCAG 4860  
Qy 4861 GGAATTCAG 4920  
Db 4861 GGAATTCAG 4920  
Qy 4921 TGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 4980  
Db 4921 TGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 4980  
Qy 4981 TGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 5040  
Db 4981 TGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 5040  
Qy 5041 TAGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 5100  
Db 5041 TAGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 5100  
Qy 5101 CAAGAGAGCTTCTGAG 5160  
Db 5101 CAAGAGAGCTTCTGAG 5160  
Qy 5161 CCGTGAAG 5220  
Db 5161 CCGTGAAG 5220  
Qy 5221 GGTCCCGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 5271  
Db 5221 GGTCCCGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 5271

RESULT 3  
US-09-985-637A-1  
Sequence 1, Application US/09985637A  
Publication No. US20030119000A1  
GENERAL INFORMATION:  
APPLICANT: Polansky, Jon  
TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PRO  
FILE REFERENCE: 13587.296  
CURRENT APPLICATION NUMBER: US/09/985.637A  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 1  
LENGTH: 5300  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-985-637A-1

Query Match 99.5%; Score 5246.4; DB 10; Length 5300;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 ATCTTTGTTCACTTACCTCAGGGCTATTATGAAATGAAATGAGTATACCAATGTGAAG 60  
DB 1 ATCTTTGTTCACTTACCTCAGGGCTATTATGAAATGAAATGAGTATACCAATGTGAAG 60  
QY 61 TCCATTAAGTGTATAGCTCCATGGATGTATGCTTTGGAGGATGATTAAGATCA 120  
DB 61 TCCATTAAGTGTATAGCTCCATGGATGTATGCTTTGGAGGATGATTAAGATCA 120  
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DB 121 GGAAGAGAGATATCCAGTATGCAAGTGTCCAGGCTGTGCTCTTATTTAGTA 180  
QY 181 CAGATGTGCTCTGACGAAAGCTATTCTTCAAGAAACATCATCAATATGTAATC 240  
DB 181 CAGATGTGCTCTGACGAAAGCTATTCTTCAAGAAACATCATCAATATGTAATC 240  
QY 241 CATCAACAGAGAGTAAAGAAACAGGAATGATGGGCACTTGCCAAAGAAAAATCCAG 300  
DB 241 CATCAACAGAGAGTAAAGAAACAGGAATGATGGGCACTTGCCAAAGAAAAATCCAG 300  
QY 301 GAGAGCAAAATATGATGAAAAATTAACCTTTCTTTTAAATTTTCAAGAAAAATG 360  
DB 301 GAGAGCAAAATATGATGAAAAATTAACCTTTCTTTTAAATTTTCAAGAAAAATG 360  
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DB 361 ATGAGGACCAAAATCAATGAAATGAAACAGCTCAAGAAAGATGTTCCAAATTGG 420  
QY 421 TAAATTAAGTATTTGCTTGGAGAGAGCTCCATGATGAGCTTGAATGGAAAAATGGAA 480  
DB 421 TAAATTAAGTATTTGCTTGGAGAGAGCTCCATGATGAGCTTGAATGGAAAAATGGAA 480  
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DB 481 AAAGCTCAAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
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QY 1141 GTGCTCAACCATTTTAAAGCTTTTAAAGCTTTTAAAGCTTTTAAAGCTTTTAAAGCTTT 1200  
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DB 1201 TGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
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DB 1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGGTTTCAAGAAATTTCTCTGCAAGCTTC 1380  
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QY 1441 GTTTCACCATATTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
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DB 1681 CACTGAGCTCACTCACTTTTCCCTCACTCACTTTTCCCTCACTCACTTTTCCCTCACT 1740  
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Db 1921 TGGGTGCTGAGACAAGCTGAGAGCCCGTGCACATGATGTTGTTTATCACTCTAG 1980  
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Db 1981 GACCTGTGCTTCTATTTCTGTGTGACTGTTCACTTCAATCCAGCATTCATTTGCAATT 2040  
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Db 2281 CCCCCAAGCCGAGTCTTCCAGAGCCCTCCCTCCATCAAGAGTCAAGAGTCAAGTCC 2340  
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Db 2521 TGGGAGAGCTGGGGCTGAGAGCGGGTGTGAAGAGCAGAAAGGAGAAAGGAGCTGAA 2580  
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 DB 4560 TATATTTTGAATAACATCTTTCTGAGAAAGTCCAGATTTCCACCAATGAGGCTTCTG 4619  
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 DB 4620 GCATGCAACACACAGAGTAAAGAACTGATTTAGAGGCTTAACATTTGATGACATTTGGTCTGAG 4679  
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 DB 4680 ATGCAAGCTGAATTTGAAAGTCTCTCCAAAGTACACAGTGTGTTTAAAGTAAAGGCT 4739  
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 DB 4800 CCTTGTGTCTGCTGCTGTATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859  
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RESULT 4  
 US-10-244-633-1  
 ; Sequence 1, Application US/10244633  
 ; Publication No. US2003068640A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nguyen, Thai D.  
 ; APPLICANT: Polansky, Jon R.  
 ; APPLICANT: Chen, Pu  
 ; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,  
 ; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related  
 ; TITLE OF INVENTION: Disorders  
 ; FILE REFERENCE: 07425.0057.US01  
 ; CURRENT APPLICATION NUMBER: US/10/244,633  
 ; CURRENT FILING DATE: 2002-09-17  
 ; PRIOR APPLICATION NUMBER: US/09/306,828  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: US 09/227,881  
 ; PRIOR FILING DATE: 1999-01-11  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: Microsoft Word 97  
 ; SEQ ID NO 1  
 ; LENGTH: 5300  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-244-633-1

Query Match 99.5%; Score 5246.4; DB 15; Length 5300;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 ATCTTGTGAGTTTACCTCAGGCTATTATGAATGAATGAATGAATGAATGAATGAATGAATGA 60  
 DB 1 ATCTTGTGAGTTTACCTCAGGCTATTATGAATGAATGAATGAATGAATGAATGAATGAATGA 60  
 QY 61 TCTATTAACCTGTAAGCCTCCATTCGATGATGATGATGATGATGATGATGATGATGATGATG 120  
 DB 61 TCTATTAACCTGTAAGCCTCCATTCGATGATGATGATGATGATGATGATGATGATGATGATG 120  
 QY 121 GGAAGAGGATATCCAGCTTACCAAGTGTCCAGGCTGTGCTGCTTATTTAGTGA 180  
 DB 121 GGAAGAGGATATCCAGCTTACCAAGTGTCCAGGCTGTGCTGCTTATTTAGTGA 180  
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Db 1381 CGCGTAGCTGGAGTACTAGAGCGAGCGCCGGCTAAATTTTGTATTTGTAGTAGAGTGG 1440  
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Db 4791 TCCATTAACCTGTAAAGCTCCATTCGGATGTAATGCTTTGGCAGGATGATAAATCA 4850  
Qy 121 GGAAGAAGAGTATCCAGCTTACGCAAGTGTCCAGGCTGTGTCTCTTATTTAGTA 180  
Db 4851 GGAAGAAGAGTATCCAGCTTACGCAAGTGTCCAGGCTGTGTCTCTTATTTAGTA 4910  
Qy 181 CAGATGTTGCTCCTGACAGAAAGCTATTTCTCAGAAAACATCATCAATATGTAAATC 240  
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Db 6591 TGAAGCCCGGAGAGGTTTCTCCTCAGCTGGGGAAGCTCAGAGCAACCGGGGCTC 6650  
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Qy 2161 GCAACTTAACCCAGTCTGAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCG 2220  
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Db 8151 AGTACCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 8210  
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Db 8869 TTTATGAGTATGCAATTTGCTTTTCTTCTGAGTTTCTTCTGAGTTTAAAGCA 8929  
QY 4199 GGGATTTATTAACCTACAGTCCAGAAAGCTGTGATTTGATGAGGAAAAATTAATTT 4259  
Db 8929 GGGATTTATTAACCTACAGTCCAGAAAGCTGTGATTTGATGAGGAAAAATTAATTT 8989  
QY 4259 TTTGTTTAAACCACTTCTTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 4319  
Db 8989 TTTGTTTAAACCACTTCTTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 9049  
QY 4319 ACTCAAGTGGTAAATTAACAGTACCTGTGATTTGCTTACCAATAGAAATCAAGACAT 4379  
Db 9049 ACTCAAGTGGTAAATTAACAGTACCTGTGATTTGCTTACCAATAGAAATCAAGACAT 4439  
QY 4379 TTTATTAATTAATTAACAGTGTGATTTGCTTACCAATAGAAATCAAGACAT 4439















TITLE OF INVENTION: Disorders  
FILE REFERENCE: 07425.0057.US01  
CURRENT APPLICATION NUMBER: US/10/244,633  
CURRENT FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: US/09/306,828  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US/09/227,881  
PRIOR FILING DATE: 1999-01-11  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 37  
LENGTH: 283  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-244-633-37

Query Match 4.3%; Score 227; DB 15; Length 283;  
Best Local Similarity 100.0%; Pred. No. 2,4e-47;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5045 AACTATTATTGGGCTATGCTGATTAATTGGGATGTTCTTTTAAAAAACTCCAA 5104  
DB 1 AACTATTATTGGGCTATGCTGATTAATTGGGATGTTCTTTTAAAAAACTCCAA 60  
QY 5105 CAGACTCTGGGAAGTTATTTCTTAGAATCTTGCTGGCAGGCTGAAGGCAACCCCTG 5164  
DB 61 CAGACTCTGGGAAGTTATTTCTTAGAATCTTGCTGGCAGGCTGAAGGCAACCCCTG 120  
QY 5165 TGCACAGCCCCACCCACCTCAGCTGCGCACTCTGCTCTCCCAATGAAGGCTGGCTC 5224  
DB 121 TGCACAGCCCCACCCACCTCAGCTGCGCACTCTGCTCTCCCAATGAAGGCTGGCTC 180  
QY 5225 CCCAGTATATATACTCTCTGAGCTCGGGGATAGACAGCAAG 5271  
DB 181 CCCAGTATATATACTCTCTGAGCTCGGGGATAGACAGCAAG 227

RESULT 13  
US-10-087-192-1225

Sequence 1225, Application US/10087192  
Publication No. US20020182586A1  
GENERAL INFORMATION:  
APPLICANT: Engelhard, David W.  
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
TITILE OF INVENTION: CANCER  
FILE REFERENCE: 52945200122  
CURRENT APPLICATION NUMBER: US/10/087,192  
CURRENT FILING DATE: 2002-03-01  
PRIOR APPLICATION NUMBER: US 09/747,377  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/798,586  
NUMBER OF SEQ ID NOS: 2059  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1225  
LENGTH: 30057  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(30057)  
OTHER INFORMATION: n = A,T,C or G  
US-10-087-192-1225

Query Match 4.2%; Score 222.6; DB 13; Length 30057;  
Best Local Similarity 56.9%; Pred. No. 1.2e-44;  
Matches 936; Conservative 0; Mismatches 564; Indels 145; Gaps 23;  
QY 2363 CTGTGATCTGAGCTGAGACTCTCTTGCTCAGGCTCCAGAAAGGAATGAGAGGGA 2422  
DB 6411 CTCTGGCTCTGCTCTCTGAGCTTCTGACTCTCTGATCCAGAAAGGATATGAGATGAA 6470

QY 2423 AACTAGTCTTAACGAGAAATCTGAGGAGGACAGTGTTCCTCAGAGGGAAGGCGCTCCA 2482  
DB 6471 AATATATCTTAACGAGAAATCTGAGGAGGAGTGTTCCTCAGAGGGAAGGCGCTCTG 6530  
QY 2483 CGTCCAGAGAAATTCAGAGAGGTGGGACTGAGAGGAGTGGGAGCGCTGAGGCTGAGCGG 2542  
DB 6531 TGTCAG---AATCCAGAGAGGTGGGCTGAGAGGAGTGGGCGCTG-----GCT 6580  
QY 2543 GTGCTAAAGGCAAGGAGTGAAGGCGCAGAGGCTGAAGCTGCCAATGTTCACTGTG 2602  
DB 6581 GCCAGAGTGAACAGGAAGGTGAAGAGG-TAATTAATCTCACCAAGGTGTCATGTGG 6639  
QY 2603 TTCAGGGGCTGGAGTTTTCGTTGCTTCTGAGCCTTTTATCTTTCTGCTTG 2662  
DB 6640 TTGCTGAGTGAAGGAGGCTCTGTTTCTCCACAGAGC-----CTTTCTGCTTA 6692  
QY 2663 GAGAGAGAGAGTCTAATTCATGAAGGATGAGCTTTATGAAGTCACTGTTAAATTC 2722  
DB 6693 GAGAGCAATGTTCTAATCTTAAGAAAGATGAGCTTATGAATCATTTGCTAAGCT 6752  
QY 2723 CAGGCTGCTGATGCTTTTCTCTTCC-T-CAAGGCTTTAATTAAGGAATAGAGAGCG 2781  
DB 6753 CAAGGCTGTTGATGTTTCCAGCACTGAAGGCTTTCATTTCTGGGATAGAGAGCA 6812  
QY 2782 AGCTCATTTCTAGGCGCTTAATTCACGAGAGAGTGAAGTCTTTTCTTCATGTC 2841  
DB 6813 AGCTCATTTCTTAGCAATTTGCTCAAGGAGAGAGTGAAGTCTTCTGACTTGA 6872  
QY 2842 TTCTGGCACTACTAGCCCTGTGTGACTTGTGCTTATGAACCGTGAACCTT 2901  
DB 6873 GACATGATGATGATTTCTCT-----GACTGTGATGTAAGAAATGT-AAAGCTTG 6923  
QY 2902 GAATAGAGAGACTCGTCTTTCTTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2961  
DB 6924 GGAATCA-----GTTTCTCTGCTGCTGCTGCTTTCATTAACCGGAGACCTGAG 6975  
QY 2962 CAAGTCTCTCTCTCTGCGGCAATGCTTCTCTGCTAATAAACCCTTGACCTCTC 3021  
DB 6976 CAA--GATTCCTCTCTCTGACCTTGAATCTCTCACTCAGAGGCGCG----- 7023  
QY 3022 GTGTTCTGTAACACTTCCCTGATTCCTGTAAGGAGGAGTGTGAAGGAGAGAG 3081  
DB 7024 -----CAGCCCAAGTGTCTGTGTGAAGAGAGAGCTGAGAGCCGTGAGAG 7069  
QY 3082 GCAGAGTGAAGAGCTGAACCAAGAGGAGTGAAGGAGCAGAGAGGAGAGAG 3141  
DB 7070 GCTGAGCTCAATCACTGAGGCTGTGAGGAGTGAAGGCTGTTGATGAGGAGAGAAAT 7129  
QY 3142 CTGGGCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 3192  
DB 7130 GTGATGCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 7189  
QY 3193 CCAATGCTTCAGAAAGCTCATGACCCCAAGCCCATTTTCTTCTCTCAAGATA 3252  
DB 7190 CCAAGTGAATGAAGAGATACAAATTAACAAGAAAC---CCCATGCTCTTCCCTTA 7247  
QY 3253 GACATGAGCAATTTGCCAATTAACCAAAAGATGCAAGACTAATGCTGTGCTTTGC 3312  
DB 7248 AGCATATATACCTGCGCAGAGAACAGAGAGAGAGAGATGCTGCTGAGC---TGTC 7304  
QY 3313 CTGGCAATTAAGAAATGCGGCAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3372  
DB 7305 CAGGTATTCAGAAATGCGGCTGAGTGAATGAG---AATGCAAGAGATGTTGCTCA 7363  
QY 3373 CCTGACAGACCCCAAGCACTGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3432  
DB 7364 CCTGAGCAGAGCCCAAGCACTGAGCAAGGCTGAG---AATATTCAGACTGAGTGA 7422  
QY 3433 CGCAGGAG 3492  
DB 7423 CTTACAGAGATGAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7473  
QY 3493 AAGGCAAGTGAATGAGCAAGAGATTAATGATCAAGTGAATCTGAGGCTTGAAGAGC 3552



